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length:

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score:

2, Appli 5, Appli 89, Appl 651, App

8, Appli 8, Appli 8, Appli 8, Appli 8, Appli 2813, Appli 3, Appli 70, Appli 70, Appli 3, Appli

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Post-processing: Minimum Match 0%
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US-09-621-976-1835

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US-09-680-683A-3

US-09-886-683A-3

US-09-663-600A-139

US-09-663-600A-139

US-09-188-930-55

US-09-312-283C-55

US-09-312-283C-55

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US-09-215-681-104

US-09-215-081-104

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Compugen Ltd.
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  sequence
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106, App
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125, Appl
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PALENT NO. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Profile REFERENCE: GENSET, 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: PALENT.DM
SEQ ID NO 1835
LENGTH: 615
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 173..511
NAME/KEY: Sig_peptide
LOCATION: 173..409
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 4.30000019073486
OTHER INFORMATION: seq YDSLLALSPDLQA/AR
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les 529; Conserv
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US-09-041-485D-5
US-09-040-838-651
US-09-641-638-651
US-07-991-8678-8
US-08-107-755A-8
US-08-544-332-8
US-09-370-861A-8
US-09-621-976-2813
US-09-621-976-2813
US-09-604-3
US-09-604-3
US-09-604-3
US-09-604-708-70
US-08-713-4198-3
US-07-867-106-2
US-07-991-867-32
US-08-107-755A-32
US-08-107-755A-32
US-08-107-755A-32
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Pred. No. 7.4e
1; Mismatches
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Result

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APPLICANT: Tang, Y. L. APPLICANT: Tang, Y. L. APPLICANT: Liu, Chenghua APPLICANT: Asundi, Vinod APPLICANT: Zhang, Jie APPLICANT: Zhang, Jie APPLICANT: Chen, Rui-hong APPLICANT: Zhao, Qing A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 784C122B

CURRENT APPLICATION NUMBER: US/09/620,312D

CURRENT FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR APPLICATION NUMBER: 09/488,725

PRIOR PILING DATE: 2000-04-25

PRIOR PILING DATE: 2000-01-21

NUMBER OF SEO ID NOS: 1105

SOFTWARE: pt Filgenes Version 1.0

SEQ ID NO 986

LENGTH: 708
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i Sequence 986, Application US/09620312D
patent No. 6569662
GENERAL INFORMATION:
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NAME/KEY: CDS
LOCATION: (46) ..(708)
IS-09-620-312D-986
                                                                                                                                                                                                                                                                     Query Match 8.7%;
Best Local Similarity 57.4%;
Matches 337; Conservative
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APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dinrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Domanac, Radoje T.
APPLICANT: Domanac, Radoje T.
TITLE OF INVENTION: No. 6559662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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                                                              126 GCTGTTTCTTGGTGGTGTTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTG 185
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Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
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AGTCGTCCTGACACTGCTGGGCTGGGTGAATGGCCTGGTCTCCTGTGCCCTGCCCATGTG
                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                         Score 175.8; DB 4; Pred. No. 3.8e-36; 0; Mismatches 247;
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TITLE OF INVENTION:
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ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,884
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,882
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/070,923
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APPLICATION NUMBER: 60/048,916
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APPLICATION NUMBER: 60/048,970
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                                                                                  GGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTGGTGGTGTTGGAATGG
                                                       GAACAATGGCCTCCATGGGGCTACAGGTAATGGGCATCGCGCTGGCCGTCCTGGGCTGGC
 TGGCCGTCATGCTGCTGCGCGCGCTGCCCATGTGGCGCGTGACGGCCTTCATCGGCAGCA
                        TGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGAGTGTCGGCCTTCATTGAAAACA
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Matches 315; Conserv
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               TGGCCGTCATGCTGTGCTGCGCGCTGCCCATGTGGCGCGTGACGGC
                                                                   GAACAATGGCCTCCATGGGGCTACAGGTAATGGGCATCGCGCTGGCCGTCCTGGGCTGGC
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PRIOR FILING DATE: 1990-02:
PRIOR APPLICATION NUMBER: 6
PRIOR FILING DATE: 1999-02:
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.
SEQ ID NO 22
LENGTH: 1665
TYPE: DNA
ORGANISM: Homo sapiens
US-09-300-958A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence 22, Application US/09300958A
Patent No. 6495319
                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/300,958A
CURRENT FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/083,331
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/098,070
PRIOR APPLICATION NUMBER: 60/098,070
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Trenkle, Thomas
TITLE OF INVENTION: Reduced Complexity Nucleic
TITLE OF INVENTION: Using Same
FILE REFERENCE: P-PH 3457
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APPLICANT: Welsh, John
APPLICANT: Trenkle, Th
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Score 158.6; DB 4;
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US-09-673-395A-71
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Best Local Similarity
Matches 314; Conserv
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CURRENT APPLICATION MEBER: US/09/673,395A
CURRENT FILLING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 637
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 71
LENGTH: 1253
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GENERAL INFORMATION:
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APPLICANT: HINZWANN, BERND
APPLICANT: SCHMITT, ARMIN
APPLICANT: PILARSKY, CHRISTIAN
APPLICANT: DAHL, EDGAR
APPLICANT: DAHL, EDGAR
APPLICANT: ROSENTHAL, ANDRE
TITLE OF INVENTION: HUWAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
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CTATGATTCCCTGCTGGCTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGC
                                   GTACAAGGGGCTGTGGATGGACTGCGTCACGCAGAGCACGGGGATGATGAGCTGCAAAAT
                                                                  CTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAAT
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NUMBER OF SEQ ID NOS: 376
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 93
LENGTH: 1722
TYPE: DNA
ORGANISM: Homo sapiens
US-09-489-847-93
                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PT/US99/17130
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-39
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/096,319
EARLIER FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
EARLIER FILING DATE: 1998-08-06
EARLIER FILING DATE: 1998-08-06
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US-09-489-847-93
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Best Local S
Matches 306
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TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: PZ031P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              543 GTACGACTCGCTGTCCGCCTGTCCGCGGCCTTGCAGGCCACTCGAGCCCTAATGGTGGT
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 CTGATCCTGGCGTGCGGGCTGCCCATGTGGCAGGTGACCGCCTTCCTGGACCACAACATC
                                                                                                          ACAGTGGCTGTCACTGTCATGCCTCAGTGGAGAGTGTCGGCCTTCATTGAAAACAACATC 216
                                                                                                                                               TCCTGGGAATGAGAGCAAGGCTGGGTACCG
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                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                     7.4%;
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Pred. No. 5.8e-29;
2; Mismatches 242; Indels
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TITLE OF INVENTION: Antibodies against SEMP1 (p
FILE REFERENCE: Case 20692
CURRENT APPLICATION NUMBER: US/09/886,683A
CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: EP01113344.6
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: EP01107799.7
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 4
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US-09-886-683A-3
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Best Local Similarity
Matches 295; Conserv
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SEQ ID NO 3
LENGTH: 3443
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GENERAL INFORMATION:
APPLICANT: Koch, Stefan
APPLICANT: Kubbies, Mani
APPLICANT: Mundigl, Olaf
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TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: (221)..(853)
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Mundigl, Olaf
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52.5%;
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                                                                                                                                                                                                                                                                                  Score 134.8; DB 4;
Pred. No. 4.2e-25;
0; Mismatches 267;
                                                                                                                                                                                                                                                                                                                                      Length
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CURRENT FILING DATE: 1998-08-07
FEARLIER APPLICATION NUMBER: US 60/058,108
FEARLIER FILING DATE: 1997-09-05
FEARLIER APPLICATION NUMBER: US 60/054,961
FEARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOPTWARE: FRASESEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 3483
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US-09-130-491-3
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APPLICANT: Holtzman, Douglas A.
APPLICANT: Goddearl, Andrew D.J.
APPLICANT: Goddearl, Andrew D.J.
TITLE OF INVENTION: TANGO-71, TANGO-73,
FILE REFERENCE: 09404/041001
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 295; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09130491 Patent No. 6416974 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORCANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (240)...(872)
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                           GCGACAACATCGTGACCGCCCAGGCCATGTACGAGGGGCTGTGGATGTCCTGCGTGTCGC
                                                                              AAAACAACATCGTGGTTTTTGAAAACTTCTGGGAAGGACTGTGGATGAATTGCGTGAGGC
                                                                                                                                  GATGGATCGGCCATCGTCAGCACTGCCCCTGCCCCAGTGGAGGATTTACTCCTATGCCG
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52.5%;
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Pred. No. 4.2e-25;
0; Mismatches 267;
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433 396 373

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GENERAL INFORMATION:
APPLICANT: ROSEN et al
ITILE DE INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: PZ031P1
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
EARLIER FILING DATE: 1998-07-30
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-08-15
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER APPLICATION NUMBER: 60/095,455
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US-09-489-847-125
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SEQ ID NO 125
LENGTH: 1380
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Best Local Similarity 55.7%;
Matches 308; Conservative
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Patent No. 6476195
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NUMBER OF SEQ ID NOS: 376
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                                                                                      ACAGTGGCTGTCACTGTCATGCCTCAGTGGAGAGTGTCGGCCTTCATTGAAAAACATC
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                                                                                                                                                                                                                                      Score 129; DB 4;
Pred. No. 8.3e-24;
                                                                                                                                                                                                                      Mismatches 240;
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US-09-663-600A-45
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PRIOR FILING DATE: 1998-11-13
PRIOR PPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-3
PRIOR PPLICATION NUMBER: 60/069,957
PRIOR PPLICATION NUMBER: 60/074,121
PRIOR PPLICATION NUMBER: 60/074,121
PRIOR PPLICATION NUMBER: 60/091,563
PRIOR PILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR PILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR APPLICATION NUMBER: 60/096,273
PRIOR PILING DATE: 1998-08-09
PRIOR PILING DATE: 1998-09-04
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SOFTWARE: Patent.pm
SEQ ID NO 45
LENGTH: 1524
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CURRENT APPLICATION NUMBER: US/09/663,600A
CURRENT FILING DATE: 2000-09-15
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                                     OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.6999980926514
OTHER INFORMATION: seg ILGLLGLLGTLVA/ML
NAME/KEY: polyA_signal
LOCATION: 1510..1515
                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                        NAME/KEY: sig_peptide
LOCATION: 160..231
                                                                                                                                                                                   FEATURE:
      NAME/KEY: polyA_site
LOCATION: 1506..1519
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US-09-663-600A-45
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Best Local Simi
Matches 319;
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OTHER INFORMATION: est
NAME/KEY: misc feature
LOCATION: 954. 983
OTHER INFORMATION: homol
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LOCATION: 39..93
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LOCATION: 1210..1489
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LOCATION: 597..846
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Pred. No. 1.1e-22;
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US-09-663-600A-139
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CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR PELLONION NUMBER: 60/066,677
PRIOR PELLONION NUMBER: 60/069,957
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR PILING DATE: 1998-02-09
PRIOR PILING DATE: 1998-04-13
PRIOR PILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
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LOCATION: 36...107
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.6999990926514
OTHER INFORMATION: seq ILGLIGLIGTLVA/ML
NAME/KEY: polyA signal
LOCATION: 1302...1307
NAME/KEY: polyA_site
LOCATION: 1389..1400
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SEQ ID NO 139
LENGTH: 1400
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GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Ba APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR
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Best Local (
                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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                           <u>ATGCCCTCTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTTCTGGGGCCTTTTGGGC</u>
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                                                                            ACACTGGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATT
                                                                                                                ACAGTGGCTGTCACTGTCATGCCTCAGTGGAGAGTGTCGGCCTTCATTGAAAACAACATC
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51.0%;
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Pred. No. 1.7e-22;
); Mismatches 305
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GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cel
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION UNMEER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 55
LENGTH: 413
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US-09-188-930-55
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Best Local Similarity
Matches 189; Conserv
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                                                                                                  TCCCTGGTGCTGGGCTTCCTGGCCATGTTTGTGGCCACGATGGGCATGAAGTGCACGCGC 140
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   ATCATCACGGGCATGGTGGTGCTCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGA
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Pred. No. 3.6e-15;
0; Mismatches 157;
                                                                                                                                                                                                                                                               Length 413;
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APPLICANT: Strachan, James D.
APPLICANT: Steeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
APPLICANT: Mumble, Krishanand D.
APPLICANT: Mumble: Compositions Isolated from Skingler Strack
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011C2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 199-05-14
MUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 55
LENGTH: 413
TYPE: DNA
ORGANISM: Mouse
US-09-312-283C-55
                                                         US-09-404-879A-104
Sequence 104, Application US/09404879A
Patent NO. 6468546
GENERAL INFORMATION:
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  GENERAL INFOR
APPLICANT:
APPLICANT:
APPLICANT:
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Mitcham, Jennifer L.
King, Gordon E.
Algate, Paul A.
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Pred. No. 3.6e-15;
0; Mismatches 157;
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Sequence 104, Application US/09338933

Patent No. 6488931

Patent No. 6488931

GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer Lynn

FITTLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF

TITLE OF INVENTION: OVARIAN CANCER

FILE REFERENCE: 210121.462C1

CURRENT FILING DATE: 1999-06-23

CURRENT FILING DATE: 1999-06-23

NUMBER OF SEQ ID NOS: 312

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 104

LENCTH: 441

TYPE: DNA

ORGANISM: Homo sapien

US-09-338-933-104
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; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FLING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 104
; ENCTH: 44
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-404-879A-104
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US-09-338-933-104
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Matches 151;
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Best Local S
Matches 151
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Local Similarity 59.7%;
nes 151; Conservative
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ALIGNMENTS

AUTHORS	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX092388	RESULT 1
Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and wood,W.I.	<pre>auxaryota; metazoa; cnordata; craniata; vertebrata; suteseostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1</pre>	Homo sapiens	Homo sapiens (human)	•	AX092388.1 GI:13444508	AX092388	Sequence 119 from Patent WO0116318.	AX092388 2010 bp DNA linear PAT 21-MAR-2001		

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841 AAATGGACCCCAAAGAAACTTTGATTTACTGTTCTTAACTGCCTAATCTTAATTACAGGA 900	781 ATGTTTTTTAACTTTACTATAAAGCCATGCAAATGACAAAAATCTATATTACTTTCTCA 840	721 TATCACACCGGAAAGAAGTCACCGAGCGTCTACTCCAGAAGTCAGTATGTGTAGTTGTGT 780	661 AACGAAAAGAGCAGTAGCTACAGATACTCGATACCTTCCCATCGCACAACCCAAAAAAAGT 720	601 TGGACCACGGCACTGGTGCTGATTGTTGGAGGAGCTCTGTTCTGCCTGC	541 TATAACTCAATAGTGAATGTTGCCCAAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGA 600	481 ACGGGCATGGTGGTGCTCATCCCTGTGAGCTGGGTTGCCAATGCCATCAGAGATTTC 540	421 GGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATC 480	361 GTGATGTCCTTCGTTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACG 420	301 TCCCTGCTGGCTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCC 360	241 GGACTGTGGATTGATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGAT 300	181 CAGTGGAGAGTGTCGGCCTTCATTGAAAACAACATCGTGGTTTTTTGAAAACTTCTGGGAA 240	121 GCTGGGCTGTTTCTTGGTGGTGTTGGAATGGTGGCACAGTGGCTGTCACTGTCATGCCT 180	61 CGGAGTCCAGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATC 120	1 GGAAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTC 60	Query Match 100.0%; Score 2010; DB 6; Length 2010; Best Local Similarity 100.0%; Pred. No. 0; Matches 2010; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/db/ /mc/ /or/	Patent: WO 0116318-A 119 08-MAR-2001; Genentech, Inc. (US) Location/Qualifiers 1 2010	Secreted and transmembrane polypeptides and nucleic acids encoding the same
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 2010)

E 1 (bases 1 to 2010)

Clark, H.F., Gurney, A.L., Abaya, B., Baker, K., Baldwin, D., Brush, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, Yuan, J., Zhang, M., Zhang, Z., The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:
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| protein_id="AGN89070.1" |
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1620	561 561	
1560	01 AGGCTATACTCAGAAGAAAAAGTGAAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAA 	
1500	441 ATTAACATTITTAAAACGCAGATATTITGTCAAGGGGGCTTTGCATTCAAACTGCT	
1440	381 TTAGAAATCCTAACTTCTTTATCCTCTTCTCCCAGAGGCTTTTTTTT	
7380 7380	.321 TAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTGTTTTTTAGCCTAGGAG	
1320	ATTAAAATGAAGGCTT ATTAAAATGAAGGCTT	
1260	1201 ACTCAACTATIGCTITTCAGGGAAATCATGGATAGGGTTGAAGAAGGTTACTATTAATTG	
1200	141 GACATGCTTATATGGTTTTATATAATGAAATGCCAGTCCATTACACTGAATAAATA	
1140	81 ATTICICCACGACATAGCATTATGTACATAGATGAGTGTAACATTTATATCTCACATAGA	
1080	021 CTCTTTTATCATTACTTCAAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTA	
1020	GGTGGTTCAAGCATCTA GGTGGTTCAAGCATCTA	
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900	1 AAATGGACCCCAAAGAAACTTTGATTTACTGTTCTTAACTGCCTAATCTTAATTACTAGGA	
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AP000884 GI:6580113
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                                                                                                     Similarity
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961 AATGCTTTGATTGTTCTAGAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAAGCATCTA 57397 AATGCTTTGATTGTTCTAAGAAGTATTTGTTTTCTAAGGTGGTTCAAGCATCTA 7 1021 CTCTTTTTACTACTTCAAAAATGACATTTGTTTTCTAAGGTGGTTCAAGCATCTA 8 1021 CTCTTTTTACTACTTCAAAAATGACATTGCTAAAAACTGCATTATTTTACTACTGCTGTA 9 1021 CTCTTTTTACCACTACATTACTTCAAAAATGACATTGCTAAAAATGACATTTATTT	121 GCTGGGCTGTTTCTTGGTGGTTTGGAATGGTGGGCAACAGTGGCTTGAATGGTTGATAGGTT b 58237 GCTGGGCTGTTTCTTGGTGGTTTGGAATGGTTGGACACAGTGGCTTGAAAAGTTCTGGAAAAGTTCTGGAAAAGTTCTTGGAAAAGTTCTTGGAAAAGTTCTTGGAAAAGTTCTTGGAAAAGTTCTTGGAAAAGTTCTTGGAAAAGTTCTTGGAAAAGTTCTTGGAAAAGTTCTTGGAAAAGTTCTTGGAAAACTTCTTGGGAAAAGTTCTTGGAAAACTTCTTGGGAAAACTACTTTGGGAAAAGTTCTTGGGAAAACTTCTTGGGAAAACTACTTTGGGAAAACTACTTTGGGAAAACTACTTTGGGAAAACTACTTTGGGAAAACTACTTTGGGAAAACTACTTTGGGAAAACTACTTTGGGAAAACTTCTTGGGAAAACTACTTTGGGAAAACTACTTTGGGAAAACTACTTTGGGAAAACTACTTTGGGAAAACTACTTTGGGAAAACTACTTTGGGAAAACTACTACTACAAAAACTACTGAAAAACTACTTTGGGAAAACTACTACAAAAAATTATGAATTTTGCTTTGTTGCTTTCTCTGGGAACCTACAAAAAAAA
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The chromosome 21 mapping and sequencing consortium consisting of RIKSN Genomic Sciences Center, Human Genome Research Group, * Sagamihara 228-8555, Japan, * e.mail: hattori@gc.riken.go.jp

* unl: http://hgp.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular Genetics (addresses see below)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               * e.mail: info-chr21@molgen.mpg.de

* URL: http://chr21.rz-berlin.mpg.de/

AL163252: Submitted (10-Apr-2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * Institute of Molecular Biotechnology, Genome Analysis, *
Beutenbergstrasse 11, D-07745 Jena, Germany,
* e.mail: gscj-submit@genome.imb-jena.de
* URL: http://genome.imb-jena.de/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * GBF, Dept. of Genome Analysis,
Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
info.genome@abf.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160-8582, Japan,
* e.mail: nshimizu@dmb-med.keio.ac.jp
* URL: http://www.dmb.med.keio.ac.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Max-Planck Institute for Molecular Genetics,
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                                                                                                             541 TATAACTCAATAGTGAATGTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGA
                                                                                                                                                                                                                                                                                               TATCACACCGGAAAGAAGTCACCGAGCGTCTACTCCAGAAGTCAGTATGTGTAGTTGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214806 GGACTGTGGATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGGTGCAAAATCTATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 GTGATGTCCTTCTTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGGGCTGTTTCTTGGTGGTGGTAGAATGGTGGCCACAGTGGCTGTCACTGTCATGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
99.9%; Score 2008.4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2009; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="Simple_repeat"
/rpt_type=TANDEM
complement(10285, .10467)
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                                                                                    /rpt_family="Simple_repeat"
/rpt_type=TANDEM
5743. .6052
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complement(6134, .6214)
/note="MIR"
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/rpt_family="LTR/MalR"
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/rpt_fype=DiSPERSED
9145. 9173
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10468..10753
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10757. 10785
/note="(TAAAA)n"
        /note="L2"
/rpt_family="LINE/L2"
/rpt_type=DISPERSED
4580 .4614
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note="(TTC)n"
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258623 GGACTGTGGATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAAAATCTATGAT 258564
                                                  The PTB1 chimpanzee BAC library was prepared from DNA isolated from cultured cells established from the blood of a single male
                                                                                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGAGTCCAGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGAAGCAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an attempt was made to resolve all sequencing problems, such compressions and repeats; all regions were covered by at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neighboring clones: RP43-006021(left) and RP43-042C06(right). Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chimpanzee.
Clones may be obtained from Asao Fujiyama and co-workers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 267172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subclone or more than one M13 subclone;
and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic_DNA"
/db_xref="taxon:9598"
/chromosome="22"
/clone="PTB-118H03"
/clone_lib="PTB1 chimpanzee BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1944; DE
Pred. No. 0;
0; Mismatches
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/organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.gsc.riken.go.jp)
VECTOR: pKS145
Sequence Quality Assessment:
                           site: http://chgc.sh.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.7%;
ilarity 98.9%;
Conservative
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Best Local Simi
Matches 1989;
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                                                                                                       213427
                                                                                                                                                                                        213426 ATATGTATGGATATATTATAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATA 213367
213546 AGGGCTATACTCAGAAGAAAAATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAA 213487
                                                                                                                                                                                                                                                                                                                      213307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BS000177 267172 bp DNA linear PRI 07-OCT-2003 Pan troglodytes chromosome 22 clone:PTB-118H03, map 22, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Chimpanzee Chromosome 22 Sequencing Consortium consists of: 
*Chinses Wational Human Genome Center at Shanghai, Shanghai, China, 
*GBF, Dept. of Genome Analysi, Braunschweig, Germany, *Institute of Molecular Biotechnology, Jena, Germany; *KRIBB Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pan troglodytes
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostom.;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (26-MAY-2003) Shengyue Wang, Chinese National Human Genome Center at Shanghai, Genomic Sequencing; No.250 BiBo Road, Zhang Jiang HI-TECH Park, Shanghai 201203, CHINA (E-mail:wangsy@chgc.sh.cn, URL.http://www.chgc.sh.cn, Tel:86-21-50801919, Pax:86-21-50801922)
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Wang,S., Cai,Z., Wang,B., Zheng,H., Zhang,Y., Zhang,X., Zhu,G.,
Lu,G., Fu,G. and Chen,Z.
Direct Submission
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*National Yang Ming University Genome Research Center, Taipei,
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DNA sequence of chimpanzee chromosome 22 and its evolutionary
implications
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*Max-Planck-Institute for Molecular Genetics, Berlin,
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The RP43 chimpanzee BAC library was prepared from DNA isolated from
cultured cells established from the blood of a single male
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                                                                                                                                                                                                                                                                                       Project
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VBCTOR: pBACG3.6
Sequence Quality Assessment:
This entry has been annotated with sequence estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in
      of Genome Analysis, Braunschweig, Germany; *Institute
r Biotechnology, Jena, Germany; *KRIBB Genome Research
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                                                                                                                                                                                                                                                                                                                             ------- Summary Statistics
Sequencing vector: pUC18+100% of reads
Chemistry: Dye-terminator Big Dye and ET; 100% of reads Assembly
program: Phrap; version 0.990329
Consensus quality: 17631B bases at least Q40
Consensus quality: 176550 bases at least Q30
Consensus quality: 176577 bases at least Q20
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                                                                                                                                                                                     Center: Chinese National Human Genome Center at Shanghai Center
                                          Center, Daejeon, Korea;
*Max-Planck-Institute for Molecular Genetics, Berlin, Germany;
*Nax-Planck-Institute of Genetics, Mishima, Japan;
*National Institute of Genetics, Mishima, Capan;
*National Yang Ming University Genome Research Center, Taipei,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an attempt was made to resolve all sequencing problems, such compressions and repeats; all regions were covered by at one
                                                                                                                                                                                                                                                                                         Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neighboring clones: PTB-118H03(left) and RP43-082J09(right).
Location/Qualifiers
1. .176580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               co-workers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25; Indels
                                                                                                                                                                                                                                              Center, Yokohama, Japan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pujiyama and
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/chromosome="22"
/clone="RP43-04206"
/clone="RP43 chimpanzee BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 96.3%; Score 1935; Di
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1984; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chimpanzee.
Clones may be obtained from Asao
                                                                                                                                              Sciences Cente
Genome Center
                                                                                                                                                                                                        code: CHGCS
Web site: http://chgc.sh.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 17
Quality coverage: 9.0x
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    *GBF, Dept. o
of Molecular
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University of Leeds, Clinical Sciences Building, St James's Hospital, Leeds, LS9 7TF, UNITED KINGDOM Location/Qualifiers
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Pred. No. 0;
0; Mismatches
                                                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db_xref="textoring 5006"
/chromosome="21"
/map="21422.1"
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23. .700
/gene="CLDN8"
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99.9%;
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Best Local Similarity 99.9
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                   TTTAAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGAAGGTTAAAATGAAGGCTT
                                                                                                                                                    TAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTGTTTTTTAGCCTAGGAG
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                                                    TITAAAAACAGCITAGGGATTAAATGTCCTCCATTTATAATGAAGGTTTAAAATGAAGGCTT
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2 (bases 1 to 1931)
Leep.T.J.
Direct Submission
Submitted (08-NOV-1999) Keen T.J., Molecular Medicine Unit,
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claudin-8; CLDNB gene.
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Homo sapiens
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601 TAGCTACAGATACTCCCATCGCACAACCCAAAAAGTTATCACACCGGAAA 660 735 GAAGTCACCGAGGGTCTACTCCCATCGCACACCCAAAAAGTTATCACACCGGAAA 660 661 GAAGTCACCGAGGGTCTACTCCAGAAGTCAGTAGTTGTGTATGTTTTTTTT	975 TCTGGAAAGTAIAGTAATTTGTTTCTAAGGTGGTTCAAGCATCTTGTTTTTTTT	1621 AAAATATGTCTTGGTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAAA

Db 1369 TAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATTTTTTTT	DIS7589 BD157589 BD157589 LOCUR BD157589 BD157589 BD157589 LOCURNAL Primer for synthesizing full-length cDNA and use thereof. ACCESSION VERSION BD157589.1 GI:27863347 FEFRENCE Home sapiens (human) ORGANISM Home sapiens (human) BURATYOTA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1890) AUTHORS Cta,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sudjyama,T., Wakamateu,A., Nagai,K. and Otsuki,T. Frimer for synthesizing full-length cDNA and use thereof HELIX RESEARCH INSTITUTE OS THOM SAPIENS (HILL-2002; BLOCOL9191363-A,12432 PD 09-UUL-2002; PF 28-UUL-2000 JP 2000280990 PF 28-UUL-2000 JP 2000280990 PF 28-UUL-2000 JP 2000280990 PF 3AITO, PI SAITO, PI SEICHI NAGAI, TETSUJ 115, CIZNI/19, CIZNI/21, CIZNS/PC CIZNIS/O9, COTKI4/47, COTKI6/18, CIZNI/130, CIZNIS/00, CIZNIS/00, CIZNIS/O0, CIZNIS/O0, CIZNIS/INSTINALINE AND	FIT CDS (150)(848). Location/Qualifiers 11890 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
294 GGACTGGGATGAATTGCGGAGGCTAACATCAGGATGCAGTGCAAAATCTATGAT 353 301 TCCCTGCTGGATGAATTGCGGAGGCTAACATCAGGATGCAGTGCAAAATCTATGAT 353 302 TCCCTGCTGGCTCTTTCTCCGGACCTACAGGCACCAGAGGACTGATGTGTGCTGCTTCC 360 361 GTGATGTCCTTTCTCCGGACCTACAGGCACCAGAGGACTGATGTGTGCTGCTTCC 413 361 GTGATGTCCTTTCTTCTCTCGGACCTACAGGCACTGAAATGACTGCTGCTTCC 413 421 GGGGACAATGAGAAGGTCAAATGACAGCCAACAGAGACTGAAATGACACAGGACGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGACGAGGAATGACAAAAAGGTGAAAGGCCAATTCTGCTGACGACGATGAATGA	181 ATGITTTTTAACTTTAACTTTAACTGAAATGACAAAAATCTATATTACTGA 840 829 ATGICTTTTTAACTTTAACTTTAACTGAAATGACAAAAATCTATTATTTCAA 888 841 AAATGACCCCAAAGAAACTTTAATTAACTGATCTTAACTATTTCAA 888 842 AAATGGACCCCAAAGAAACTTTCAATTACTGTTCTTAACTGCCTAATTACAGGA 940 943 AAATGGACCCCAAAGAAACTTTCAATTACTGTTCTTAACTGCCTAATTACAGGA 948 901 ACTGTGCATCAGCTATTTATGATTTCAATTACTGCTCTTAATTACAGGA 948 902 ACTGTGCATCAGCTATTTAATTAATTCAATTACTTCATTAATTA	AGGCTT AGGCTT TAGGAG

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	AK022269 AK022269 LOCUS DEFINITION Homo sapiens CDNA FLJ12207 fils, clone MAWMA1000956, highly similar to Homo sapiens CLDN8 gene for claudin-8. ACCESSION AK022269.1 GI:10433628 KEYWORDS Oligo capping; fils (full insert sequence). Homo sapiens (human) OKGANISM Homo sapiens (human) CRGANISM RATYOLA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugano,S., Shiratori,A., Suzuki,Y., Nighikawa,T., Nagai,K., Sagano,S., Shiratori,A., Sudo,H., Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
Duesy Match Bast Local Similarity 99.4%; Pred. No. 0; Similarity 99.4%; Pred. No. 0; Mismatches 131; Conservative 0; Mismatches 14 GABANACCTCTCTCTCTCTCCCCCCCCCCCCCCCCCCCCCC	OY 781 ATGITITITAACTITACTATAAGCCATGCAAATGACAAAATCTATATTTCTCA 840 B29 ATGITITITAACTITACTATAAGCCATGCAAATGACAAAATCTATATTTCTCA 840 B41 AAATGGACCCCAAAGAAACTITGATTTACTGTTCTTAACTGCTTAATTACAGGA 900 B89 AAATGGACCCCAAAGAAACTTTGATTTACTGTTCTTAACTGCCTAATCTTAATTACAGGA 948 901 ACTGGCATCAAGAAACTTTGATTTACTGTTCTTAACTGCTAATCTTAATTACAGGA 948 902 AAATGGACCCCAAAGAAACTTTGATTCTATAAGCTATTTCAGCAGAATGAGATATACAGGA 948 903 AAATGGACATCAGAATTTATGATTCTATAAGCTATTTCAGCAGAATGAGATATTAAAATCC 1008 904 ACTGTGCATCAGCTATTTATGATTCTATAAGCTATTTCAGCAGAATGAGATATAAATTC 1000 905 AATGCTTTGATTGTTCTAGAAAGTATTTTTTTTTTTTTT

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Ono, Y., Takiguchi, S., Matanabe, S., Kimura, K., Murakami, K.,
Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A.,
Nakamura, Y., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T.
NEDO human cDNA sequencing project
Unpublished

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MI 240 GGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGGGGGGAATCATCTTCATCATC ACGGGCATGGTGCTCATCCCTGTGAGCTGGCTTGCCAATGCCATCATCAGAGATTTC 540 GGAAAAACTGTTCTCTTCTGTCGCACAGAGAACCCTCCTTCAAAGCAGAAGTAGCAGTTC 60 CGGAGTCCAGCTGGCTAAAACTCCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATC 120 173 GCTGGGCTGTTTCTTGGTGGTGTTGGTGGCGCACAGTGGCTGTCACTGTCATGCCT 180 233 GGACTGTGGATGAATTGCGTGAGGCAAGCTAACATCAGGATGCAGTGCAAAATCTATGAT 300 TCCCTGCTGGCTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCC 360 GTGATGTCCTTCTTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACG 420 414 GIGALGCCCTTCTTGGTCTTCTTGATGATGGCCATCCTTGGCATGGAATGCACCAGGTGCAGG 473 ACGGGGARGGTGGTGATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTC 593 CAGTGGAGAGTGTCGGCCTTCATTGAAACAACATCGTGGTTTTTGAAAACTTCTGGGAA Query Match

89.7%; Score 1802; DB 9; Length 1890;
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Matches 1831; Conservative 0; Mismatches 5; Indels 6; Gaps misc_feature 294 (421 474 481 181 234 241 301 361 121 54 61 TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL FEATURES COMMENT 8 8 8 8 8 g S B g 8 8 8 QQ ò ∂

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TATAACTCAATAGTGAATGTTGCCCAAAAACTAATAACCCAAAAAAAA	TGGACCACGGCACTGGTGCTGATTGTTGGAGGA 	aacgaaaagagcagtagctacaga 	TATCACACCGGAAAGAAGTCACCGAGCGTCTA	ATGTTTTTTTAACTTTACTATAAAGC	CAAAGAAACT: CAAAGAAACT:	rtctataag rtctataag	atagtaat atagtaat	TITITAICAITIACITCAAAAIGACAITG 	acatagcattatgi acatagcattatgi	CTTATATGGTTTTATTTAAAATGAA 	itgcttttcagggaatcatgg 	1 TTTAAAAACAGCTTAGGGATTAATGTCCTCCA:	1 TAATCAGCATTGTAAAGGAAATTGAATGGCTT" 	1 TTAGAAATCCTAACTTCTTTATCCTCTTCTCCCAGAGGC-TTTTTTTTTT	O AATTAACATTTTTAAAACGCAGATATTTTGTC 	O CAGGGGTATACTCAGAAGAAGATAAAAGTGTV	O PAGIGARATATTITGITITGIATTIGATTIGAGG 	O TATATGTATGGATATATTTAATAAGTATTTG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE (bases 1 to 1700)

Strausberg, E.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schwutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                               1788
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Homo sapiens claudin 8, mRNA (CDNA clone MGC:61830 IMAGE:4606880),
complete cds.
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Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
1729 AAATAAAAGAGCAGAAAAATATGTCTTGGTTTTCATTTGCTTACCAAAAAAACAACAACA
                                                                                                                                                                                                              1789 AAAAAGTIGICCTTIGAGAACTICACCIGCICCTAIGIGGGGACCIGAGGCAAAATIGI
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLOWTECH
CDNA Library Preparation: CLOWTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing Dy: National Institutes of Health Intramural
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AUTHORS
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JOURNAL
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Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDwell, J., Pearseon, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                found
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WHERGLMMOVTRQANIRMOKKIYDSLLALSPDLQAARQLMACASVWMSFLAFWMAILGM
KCTR.TGDNEKVKAHILLINGCKIYDSLLALSPDLQAARQLMACASVWASPLAF
KCTR.TGDNEKVKAHILLINGGALPFCCVPCCNEKSSSYRVSIPSHFTDQKSYHTGKKSPSV
                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Sexies: IRAL Plate: 48 Row: d Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21314655. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTGGTGGT
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yo da	16 16	1642 TAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAA
RESULT BCO208 LOCUS DEFINI ACCESS VERSIO KEYWOR	RESULT 14 BC020866 LOCUS DEFINITION ACCESSION KEYWORDS	BC020866 Homo sapiens claudin 8, mRNA (cDNA clone MGC:24067 IMAGE:4594155), complete cds. BC020866 BC020866.1 GI:18089189 MGC. Homo sapiens (human)
REFI	Z Z Z	Homo sapiens Bukarydra, Hetazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukarydra, Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1835) Strausbergs, L., Faingold, E.A., Grouse, L., Derge, J.G., Klausner, R.D., Collins, E.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
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i≓ ———	TITLE	BUTCETITEIQ, 7.5., AZZWWIBKI, M.1., SKALEKA, D., SHRAILE, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse of Mi seminores
P 2 2	JOURNAL MEDLINE PUBMED	numin and modes Corr. Sci. U.S.A. 99 (26), 16899-16903 (2002) 22388257 12477932
A E E D	AUTHORS TITLE JOURNAL	As Strausberg R. Strausberg R. Direct Submission AL Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
C C C M	REMARK COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue procurement: CLONTECH CDNA Library Preparation: CLONTECH CDNA Library Preparation: CLONTECH CDNA Library Parayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.
· ·		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov/Series: IRAL Plates: 36 Row: e Column: 23 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21314655.

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241 GGACTGTGGATGATTGCGTGAGGCTAACATCAGGATGCAGTGCAAAATCTATGAT	Oy 1321 TA 	TAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTGTTTTTTAGCCTAGGAG 1380
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OY 481 ACGGCATGGTGGTCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTC 540	1350	0.4
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Db 554 TATAACTCAATAGTGAATGTTGCCCAAAAACGTGAGGAGAAAGTTCTGTACTTAGGA 613		

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order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
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* NOTE: This is a 'working draft' sequence. It currently consists of 56 conties. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the conties are represented as * uns of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence * as soon as it is available and the accession number will
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11020: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AP001846 191923 bp DNA linear HTG 30-MAY-2000 Homo sapiens chromosome 18 clone RP11-796C24 map 18q22, WORKING DRAFT SEQUENCE, 56 unordered pieces.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Mania, Ishi, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Published Only in Database (2000)

Chases I to 191923

Attori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
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------ Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
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Homo sapiens (human)
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SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 15 AP001846

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61 GGAAAACTGTTCTTCTTGTGGCACGAGAACCCTGCTTCAAAGCAGAAGTTC 113 61 CGGAAAACTGTTCTTCTTGTGGCACGAGAACCCTGCTTCAAAGCAGAAGTTC 113 114 GGAGTCCAGCTGGTTAAACTCATCCCAGAGATAATGCCAACCCATGCCTTAGAAATC 173 115 GCTGGGCTGTTTCTTGGTGGTGTTGGAATGGTGGGCAGTGGCTGTCATGCT 180 117 GCTGGGCTGTTTCTTGGTGGTGTTGGAATGGTGGCACGTGGCTTGTCATGCT 180 118 CAGTGGAGAGTTCTTGGTGGTGTTGGAATGGTGGCACGTGGCTTGTCATGCT 180 119 GCTGGGCTGTTTCTTGGTGGTGTTGGAATGGTGGCACGTGGCTGTCATGCT 180 110 GCTGGGCTGTTTCTTGGTGGTGTTGGAATGGTGGCAGTGGCTGTCATGCT 233 181 CAGTGGAGAGTTCTTGGTGAAAACAACATCGGTTTTTTGAAAACTTCTGGGAA 293 182 CAGTGGAGAGTGTGGAGCAGACAACATCGGGTTTTTTGAAAACTTCTGGGAA 293 183 CAGTGGAGAGTGTGGAGCAGACAACATCGGTTTTTTGAAAACTTCTTGGT 300 184 GACTGTGGATGAAACAACATCGGGATGATGAAATCTATGAT 353 185 TCCCTGCTGGCTTTTCTCCGGAGCCTACAGGCACAACATGATGAAAATCTATGAT 353 186 TCCCTGCTGGCTTTTCTCCGGACCTACAGGCACCAAGATGATGTTGTGTGTG	414 GIGAIGCCTICITGGCTITCAICAIGAAGGCCAICCTIGGCATGAAAIGCACCAGGIGCACG 473	GGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATC ACGGGCATGGTGGTGATCCTTCTGTGGGGTTGCCAATGATCATCATCATC ACGGGCATGGTGGTGCTCATCCCTGTGAGCTTGGCGATGCCAATGATCATCAGAGATTTC ACGGGCATGGTGCTCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTC		661 AACGAAAAGGCAGTAGCTACGATACTCGATACCTTCCCATCGCACAACCCAAAAAGT 720	80 TATG 783 34 NATG 837 BG674625 754 bp mRNA 1	602620674F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:474618 mRNA sequence. mRNA sequence. mR674625 BG674625.1 GI:13906021 EST. Homo sapiens (human) Homo sapiens (human) ENARYOCE: Metazoa; Chordata; Craniata; Vertebrata; Euteleostc	Catarrhini, Hominidae; v/. Mammalian Gene Collec h.D.
8 3 8 3 8 3 8 3 8 3 8 3	d 5		\$ 8 \$ 8	\dagger \dagge	Qy Db RESULT 2 BG674625 LOCUS	DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT
BCC51870 Homo sapi AY401126 Mus muscu CF795832 892028 Ma BJ525963 BJ52563 BJ68453 BJ489453 BJ011735 BJ68453 BJ011735 BJ61865 BJ518862 BJ518865 BJ518862 BJ518865 BJ518765 BJ498785 AY401124 Homo sapi BM40185 BJ51865 BJ797541 BJ797541 BJ797641 BG54864 602578429 CF999695 AGENCOURT BG068381 H3064402- BE478184 162319 BB478184 162319 BB912500 601661129 CD508551 CDA91-E03 BB648933 BB648933 BB648933 BB648933 BB648933 BB648933 BF47755 AGENCOURT	178	mRNA linear EST 01-AUG-2002 A clone MAMMA1000956 5', mRNA	Vertebrata; Euteleosto ; Hominidae; Homo. ., Saito,K., Kawai,Y.,	ura,Y., Nagal,T., Sugano,S. and -0812, Japan	end one pass sequencing: Helix construction: Department of cience, University of Tokyo, and	ns" gland" 7 <u>13</u> "	DB 9; Length 837; 3.9e-142; hes 8; Indels 1; Gaps 1; ACCCTGCTTCAAGCAGAAGTAGCAGTTC 60
209.4 10.4 1804 11 BCO51870 208.6 10.4 674 29 7795132 208 10.3 689 12 BJ525963 207.4 10.3 619 12 BJ725963 207.4 10.3 619 12 BJ7187553 207.4 10.3 619 12 BJ7187553 206.4 10.3 619 12 BJ7187553 206.4 10.3 619 12 BJ7187553 206.4 10.3 654 29 AY401185 206.4 10.1 629 12 BJ79185 203.4 10.1 878 12 BJ79185 200.6 10.0 629 12 BJ79185 200.6 10.0 629 12 BJ791858 201 10.0 780 14 CF99695 201 10.0 867 10 BG781881 198.8 9.9 650 12 BJ7191 198.8 9.9 657 10 BG718638 196.4 9.7 7724 10 BG8133 194.4 9.7 724 10 BG8133 194.5 6 611 10 BF77553	ALIGNMENTS	AMMA1 Homo s	1 GI:10937 ens (human) ens Wetazoa; Butheria; 1 to 837)	Yamanoto, J., Wakamatsu, A., Nakamura, Y., Nagal, T., Sugano, S. and Isogai, T. HRI human cDNA project Unpublished (2000) Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarauu, Chiba 292-0812, Japan Tel: 81-438-52-3975	Fax: 81-438-52-3986 Email: genomics@hri.co.jp Hri human cDNA project; 5'- £ 3'- Research Institute; cDNA library Virology, Institute of Medical Sc Helix Research Institute.	/organism="Homo sapiens" /mol type="mRNA" /db_xref="taxon:9566" /clone="NAMMA1000556" /tissue_type="mammary gla /clone_lib="NAMMA1" /note="Vector: pME18SFL3"	ch 37.9%; Score 761; DB 9; Length 837; 18 Simijarity 98.9%; Pred. No. 3.9e-142; 775; Conservative 0; Mismatches 8; Indels 1; Gaps 1 GGAAAACTGTTCTTCTTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTTC
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		AU121779 LOCUS DEFINITION	VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	TITLE JOURNAL COMMENT	FEATURES SOUTCE	ORIGIN	Query Match Best Local S Matches 775 Qy 1

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/u.v./.
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//wol_type="mRNA"
//wol_type="mRNA"
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/ clone=intaxge:460680"
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/ clone lib="NTH MGC 75"
/ clone lib="NTH MGC 75"
/ note="lorgan: kidney" vector: pDNR-LIB (Clontech); Site_l:
/ force="lorgan: kidney" vector: pDNR-LIB (Clontech); Site_l:
/ sfil (ggocgctcggcc); Site 2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-ATTCTAGGGCGGGGGGGCGATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb): 15/15 colonies contained inserts
by PCR. This library was enriched for tull-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Low nowno saplens.

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Butheria, Primates, Catarrhini, Hominidae, Homo.

El (bases 1 to 72)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LiNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

http://mage.lln.gov

Plate: LLCM1346 row: g column: 09

High quality sequence stop: 735.

Location/Qualifiers

LICCALIAN ARTER 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG426438 172 bp mRNA linear EST 14-MAR-2001
602492836F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4606880 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
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                                                  Arcicacaragagacargerrarargerrirarriraaaargaaargecagrecarracae 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 TCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTGGTGGTGTT
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                                                                                                                                                           TGAATAAATAGAACTCAACTATTGCTTTTCAGGGA 1223
                                                                                                                                                                                                                                               TGAATAAATAGAACTCAA-TATTGCTTTTCAGGGA 754
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
BG426438
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Jears Adult"

Jab host="Adult"

Jab host="DH10B (Life Technologies) (T1 phage resistant)"

Jelon | Lib="UI-CF-ENI"

Jelon | Login | Lo
                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ULCF-EN1-adg-i-18-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         703 AGCATIGIAAAGGAAATIGAAIGGCITICIGAIAIGCIGITITITAGCCIAGGAGTIAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1446 CATITITAAAACGCAGATATITIGICAAGGGGCTITIGCATICAAACTGCTTTTCCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1506 TATACTCAGAAGAAGAAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523 TATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1566 AAATATTTTGTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            463 AAATATTTTTGTTTTTGTATTGAAGAATGATGCATTTTTGACAAGAAATCATATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1686 AAGAGCAGAAAAATATGTCTTGGTTTTCATTTGCTTACCAAAAAAACAACAACAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.0%; Score 683.4; DB 14
ilarity 99.9%; Pred. No. 1.4e-126;
Conservative 0; Mismatches 1;
                                                                                                             1. .703
/organism="Homo sapiens"
                                                                    Location/Qualifiers
Seq primer: M13 FORWARD POLYA=Yes.
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Best Local Similarity
Matches 684; Conserv
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                                                                    FEATURES
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McCray Lab
University of Iowa
2024 University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
2024 University of Iowa
2024 University of Iowa
2024 University of Iowa
2024 University of Iowa
2024 Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
refellowing repetitive elements were found in this cDNA
sequence: 1-58, >AT_rich#Low_complexity (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CB851106 703 bp mRNA linear EST 22-APR-2003 UI-CF-EN1-adg-i-18-0-UI.S1 UI-CF-EN1 Homo sapiens cDNA clone UI-CF-EN1-adg-i-18-0-UI 3', mRNA sequence.
                                                                                                                                 300
                                                                                                                                                                                                     384
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Bonaldo, M. F., Lennon, G. and Soares, M. B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAAAACGTGAGCTTGGAGAAAGCTCTTACTTAGGATGGACCACGGCACTGGTGGTGATT
   GAAAACAACATCGTGGTTTTTTGAAAACTTCTGGGAAGGACTGTGGATGAATTGCGTGAGG
                                                                       CAGGCTAACATCAGGATGCAAAAATCTATGATTCCCTGCTGGCTCTTTCTCCGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTGGAGGAGCACTCTGTTCTGCTGCGTTTTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 659 TACTCGATACCTTCCCATCG-ACAANCCAAAAAGTTATCACACCGGAAAGAGTCACCG
                                                                                                                                 241 CAGGCTAACATCAGGATGCAGAGCAAATCTATGATTCCCTGCTGGCTCTTTCTCCGGAC
                                                                                                                                                                                                  CTACAGGCAGCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTCTTGGCTTTCATG
                                                                                                                                                                                                                                                                                                                                ATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACATTOTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGGTCATCCCT
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
L. Submission
L. Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
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Clark, A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. 9 103 TITGIGICGACGICTGICTIAAAAAAAAGAATGIGITCTAITIGCITIATACAITIAAA 44 97 ATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTGGTGGTGTTGGAATGGTGGGC 1 ATGCCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTGGTGGTGTTGTTGGTGGTGGT 678 bp DNA linear GSS 15-DE. Homo sapiens CLDN8 gene, VIRTUAL TRANSCRIPT, partial sequence. AX400665 ; 0 Query Match
33.7%; Score 678; DB 29; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.7e-125;
Matches 678; Conservative 0; Mismatches 0; Indels Science 302 (5652), 1960-1963 (2003) TAATAAATIGIACATITITICIAATI 2010 TAATAAATIGTACATTTTTTTTAATT 19 <1. . . >678
/gene="CLDN8"
/locus_tag="HCM0633" AY400665.1 GI:39756654 Homo sapiens (human) Homo sapiens 14671302 1986 43 VERSION KEYWORDS SOURCE ORGANISM DEFINITION REFERENCE AUTHORS JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL RESULT 5 AY400665 LOCUS ACCESSION FEATURES TITLE COMMENT ORIGIN g δ 셤 δ ò à d ò a ò

41 AGAGGACTGATGTGCTGCTTCCGTGATGTCCTTCTTGGCTTTCATGATGGCCATCCTT 300	97 GCCATGAAATGCACCAGGTGCACGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTG 456	57 ACGGCTGGAATCATCATCATCACGGGCATGGTGGTGCTCATCCTGTGAGCTGGGTT 516	1.7 GCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAATGTTGCCCAAAAACGTGAG 576	577 CTTGGAGAACTCTCTACTTAGGATGGACCACGGCACTGGTGCTGATTGTTGGAGGAGCT 636	137 CTGTTCTGCTGCGTTTTTTGTTGCAACGAAAGAGCGGTAGCTACAGATACTCGATACCT 696	697 TCCCATCGCACAACCCAAAAAGTTATCACACCGGAAAGAAGTCACCGAGGGTCTACTCC 756		BG402103 No 602465638F1 NIH_MGC_75 Homo sapiens CDNA clone IMAGE:4593920 5', mRNA sequence. BG402103 BG402103.1 GI:1329551 EST. 12-WAK-2001 BG402103.1 GI:1329551 Homo sapiens (human) M Homo sapiens (human) N Homo sapiens (human) Contact: Robert Strausberg, Ph.D. Email: cgapps-r@mail.nih.gov/. Contact: Robert Strausberg, Ph.D. Contact: Robert Strausberg, Ph.D. Email: cgapps-r@mail.nih.gov/. Contact: Robert Strausberg, Ph.D. Contact: NA.G.E. Consortium/Link at: north at: http://mage.lln.gov/ Plate: LLCM134 row: k column: 09 High quality sequence stop: 599. Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Anol type="mmxna" Adaptors were used in Cloining as follows: 5' adaptor sequence: 5'-CACGGCCATARGGCC3' and 3' adaptors pare 1.5' Conf. Gand N = A, C, C, G, Or T), Abergee inserts = 1.5 Kb (range 0.5-4.0 kb). 15/15 colonies contained inserts = 2.5 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
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Tissue Procurement: Cullinguage.

Emmert-Buck, M.D., Ph.D.

cuba Library Preparation: M. Bento Soares, Ph.D.

cuba Library Preparation: M. Bento Soares, Ph.D.

cuba Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:

www-bio.llnl.gov/bbpf.image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 444.
                                                                                                                                                                                                                                                                                                                   /lab_host="DHIOB"
/clohe_lib="NCI_CGAP_Kidl1"
/note="Organ: Kidney; Site1: Not I; Site2: Eco RI;
a modified polylinker; Site1: Not I; Site2: Eco RI;
Plasmid DNA_from the normalized library NGI_CGAP_Kid3 was.
Plasmid DNA_from the normalized library NGI_CGAP_Kid3 was.
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5.000 clones made from the same library
(cloneIDS 1322376-1323911, 1456007-1456775, and
1500552-1520855). Subtraction by Bento Soares and M.
Fatima_Ronaldo.
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/clone="IMAGE:2694358"
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          by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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0; Mismatches 4;
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Contact: Robert Strausberg, F
Email: cgapbs-r@mail.nih.gov
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Unpublished (1997)

Conteat: Robert Strausberg, Ph.D.

Email: gapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:

info@image.llnl.gov

High quality sequence stop: 467. /organism="Homo sapiens"
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/db _xref="taxon:9606"
/db _xref="taxon:9606"
/db _xref="taxon:9606"
/db _xref="taxon:9606"
/db _xref="taxon:9606"
/dlone="topios"
/dlone="to briy5920 544 bp mRNA linear EST 03-NOV-2000 7087c12.Xl NCI_CGAP_Kidll Homo sapiens cDNA clone IVAGE:3643390 3', mRNA sequence. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 544)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), BF195920 BF195920.1 GI:11083309 Homo sapiens (human) RESULT 8 BF195920/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT FEATURES

1243 1064 ATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAGTGTAACA 1123 1124 TITATATCTCACATAGAGACATGCTTATATGGTTTTATATAAATGAAATGCCAGTCCAT 1183 1244 AAGGITACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGAA 1303 1304 GATTAAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCT 1363 425 424 TACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTGAAG 365 544 ATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAGTGTAACA 485 364 AAGGTTACTATTAATTGTTTAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGAA 305 1184 TACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTGAAG 0; Gaps Query Match 27.0%; Score 542.4; DB 10; Length 544; Best Local Similarity 99.8%; Pred. No. 2.6e-98; Matches 543; Conservative 0; Mismatches 1; Indels 0; g g g δ ò ò ð 셤

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Query Match 26.9%; Score 541; DB 10; Length 547; Best Local Similarity 100.0%; Pred. No. 4.9e-98; Matches 541; Conservative 0; Mismatches 0; Indels

/dlone="IMAGE:1314947"
/dlone="IMAGE:1314947"
/dlone bote="DH10B"
/dlone lib="NOI GAP Kid11"
/dlone lib="NOI GAP Kid11"
/dlone lib="NOI GAP Kid11"
/dlone lib="NOI GAP Kid11"
/dlone lib="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: NoI 1; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridication reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(clonelDs 1322376-1323911, 1456007.1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo. Contact: Robert Strausberg, Ph.D.

Email: cgapbe r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML, send email to:

info@image.llnl.gov DELIYBUYZ 547 bp mRNA linear EST 03-NOV-2000 hr81h10.x1 NCI_CGAP_Kidil Homo sapiens cDNA clone INAGE:3134947 3', mRNA sequence. 1483 1484 ATTCAAACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAA 1543 184 TITITCTIGIGIAITAAAITAACAITITIAAAAAGCAGATATITIGICAAGGGGCTITGC 125 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 547)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP); Tumor Gene Index
Unpublished (1997) 244 GITITITAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCCAGAGGCTTTT /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" High quality sequence stop: 472. Location/Qualifiers BF196092.1 GI:11083657 Homo sapiens (human) Homo sapiens FEATURES

us-10-063-732-119.rst

/Qualifiers n="Homo sapiens" == mRNA. == mRNA. NAMA1000956" NAMA1000956" LYPE="mammary gland" b= "MAMMA1" The score 535.8; DB 9; Length 577; The score 535.8; DB 9; Length 577;	562; Conservative 265 AAAACAGCTTAGGGATTAA 577 AAAANCAGTTAGGNATTAA 325 CAGCATTGTAAAGGAAATT 517 CAGCATTG-AAAGGAAATT 518 AAATCCTAACTTGTTATC	Db 458 AAAICCTAACTICTICTICTICTICTICTICTICTICTICTICTICTIC	1564 GAAATATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	158 AAAAGACAGAAAATAIGICTIGGTTTTCATTTGCTTACCAAAAAACAACAAAAAA 1744 AAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATGTCATT 1111	RESULT 11 CB851224 LOCUS LOCUS LOCUS DEFINITION UI-CF-DUI-adn-j-21-0-UI.S1 UI-CF-DUI Homo sapiens CDNA clone ACCESSION UI-CF-DUI-adn-j-21-0-UI.S1 UI-CF-DUI Homo sapiens CDNA clone UI-CF-DUI-adn-j-21-0-UI.S1 UI-CF-DUI Homo sapiens CB851224 VERSION CB851224 CB85124 CB851
1470 TCAAGGGGCTTTGCATTCAAACTGCTTTTCCAGGGCTATACTCAGAAGAAAGA	Qy 1650 TGAGTACAGACTTTGAGGTTTCATCAATATAAAAAAAAAA	QY 1830 TCTTGTACCATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTGTATTTTTCTGTTTAT 1889 Db 187 TCTTGTACCATTTCTGTTTAGTTTTACTATTGAAAATCTGTAAAATCTGTAAATTTTTCTGTTATT 128 QY 1890 TCCAAATTTGATGAAACTGACAATCCAATTTGAAAGTTTGTGTCGACGTCTGTCT	AAAIGAATGIGITCAATTACATTATAATAATAATGAATGIACATTATTATAATAATAATAATAATAATAATAATAATAAT	DEFINITION AU147533 MANMAI Homo sapiens cDNA clone MAMMA1000956 3', mRNA cequence. ACCESSION AU147533.1 GI:11009054 KEYWORDS FORT OF AU147533.1 GI:11009054 KEYWORDS Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens Enkaryota, Metazza, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AUTHORS Year I. (1977), Your Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Authors Yamamoro. J., Wakamatsu, A., Ozawa, M., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.). TITLE STATE Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Ozawa, M., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura, Y., Nagai, T., Sugano, S., Isogai, T.) JOURNAL Unpublished (2000) COMMENT Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-396 Eax: 81-438-52-396 Email: genomics@hri.cojp HRI human cDNA project; 5- & 3'-end one pass sequencing: Helix Research Institute; CDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

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Homo sapiens
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// organism="how saplens"
// orbanism="how saplens"
// clone="ut="cr-Dul-adn-12-0-UI"
// tissue_type="rrimary Lung Epithelial Cells"
// dev_stage="Adult"
// lab_host="bulloB (Life Technologies) (T1 phage resistant)"
// lab_host="bulloB (Life Technologies) (T1 phage resistant)"
// lab_host="bulloB (Life Technologies) (T1 phage resistant)"
// clone lib="Ut-CF-DUI"
// clone lib="Ut-CF-DUI"
// note="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR 1; Site 2: Not 1;
UT-CP-DUI is a normalized CDNA library containing the
following tissue (8): Primary Lung Epithelial Cells The
following tissue (8): Primary Lung Epithelial Cells The
following tissue (8): Primary Lung Epithelial Cells The
following a constructed according to Bonaldo, Lennon and
Soarse Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT773-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is GGCTGTAGGC.
TAG_SEQ=None found"
                                                                                      University of Iowa
University of Iowa
University of Iowa
2024 University of Iowa
Tels: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
Seq primer: M13 FORWARD
POLYA=No.
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                             location/Qualifiers
                                                    Contact: McCray, PB
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 586)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvahlo, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., dooliveira, P.-S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tell 1923...
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome This sequence was derived from the following URL Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/s/gethtml2.pl?tl=PMO&t2=PMO-CT0802-050301-002-c03&t3=2001-03-05&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence start: 10
High quality sequence stop: 586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    586 bp mRNA linear EST 12-JUN-2001
BMO-CT0802-050301-002-c03 CT0802 Homo sapiens cDNA, mRNA sequence.
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BG957666.1 GI:14375837
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
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/lab host="DHIOR"
/lab host="DHIOR"
/cope lib="NCI CGAP Kid11"
/note="Ocgan: Kidney; Vector: pT713D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NGI CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5.000 clones made from the same library
(cloneIDS 1322376-1323911, 1456007-1456775, and
history Society Socie
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1. (Dases 1 to 68)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Cupublished (1999)
Contact: Robert Strausberg, Ph.D.
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Www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 462.
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TITIACTACTGIAATTICICCACGACATAGCATTATGIACATAGATGAGTGTAACATTTA 97
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1 (Dases 1 to 513)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
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Emall: Gagabs-r@mall.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                           TATTACTTTCTCAAAATGGACCCCAAAGAAACTTTGATTTACTGTTCTTAACTGCCTAAT
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Catarrhini; Hominidae; Homo.
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24.6%; Score 494; DB 29; 183.0%; Pred. No. 1.2e-68; iive 0; Mismatches 115;
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14671302
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/locus_tag="HCM0633"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CicONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LiNL)
DNA Sequencing by: Incyte Genomics, Inc.
follone distribution: MGC clone distribution information can by
found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LicCMI065 row. b column: 07
High quality sequence stop: 676.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.1%; Score 505.2; DB 10; Length 689; Best Local Similarity 95.8%; Pred. No. 6.9e-91; Matches 638; Conservative 0; Mismatches 13; Indels 15;
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VIRTUAL TRANSCRIPT, partial sequence,
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tanenbaum, D.M., Civello, R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.U., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 ACAGTGGCTGTCACTGTCATGCCTCAGTGGAGAGTGTCGGCCTTCATTGAAAACAACATC 216
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Clark, A.G., Glaznowski, S., Nielson, R., Thomas, P., Kejariwal, A., Toda, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                       277 AGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTTTCTCCGGACCTACAGGCAGCC
1 Arescanceracscreteranarescreterecretresissimostrescanssers
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Best Local Similarity 99.8<sup>3</sup>
Matches 481; Conservative
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1 (basea 1 to 492)

1 (basea 1 to 492)

1 NGI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

1 NGI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

1 NGI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

2 NGI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

3 NGI-CGAP (1997)

4 Contact: Robert Strausberg, Ph.D.

5 Email: Gapbs-r@mail.nih.gov

7 The sequence contained an oligo-dr track that was present in the oligonic electide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:

1 www-bio.llnl.gov/bbry/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_Lype="marka" | marka" | mol_Lype="marka" | mol_Lype="mol_Lype="marka" | mol_Lype="marka" | mol_Lype="ma
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UI-H-BII-aem-g-01-0-UI.sl NCI CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2720040 3', mRNA sequence.
                                     CGAGGACTGATGTGTGCTGCGTCCGTCTTGGCTTTCTTGGCTTTCATGACCATCCTC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAGCCGGAATCATCTTCATCACGGCTTGGTTGTGCTCATCCCTGTCAGCTGGGTT
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                                                                                                                                                                                              GGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTG
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Homo sapiens
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CF766535 681 bp mRNA linear EST 17-OCT-2003 582003314 Bos taurus skin cDNA library Bos taurus cDNA clone CCL003314 5', mRNA sequence.
                                                                                                        480
                                                                                                                                                           GITGIGIATGITITITIAACTITIACTATAAAGCCATGCAAATGACAAAATCTATATTAC 833
                                                                                                                                                                                                                                                                    834 TITCICAAAAIGGACCCCAAAGAACTIIGAITIACIGIICIIAACIGCCTAAICIIAAI 893
                                                                                                                                                                                                                                                                                                   361 CTGTTGCCATGAAAAGAGCAGTAGCTACAGATACTCCATACCGTCCCACCGAACAACCA 420
                                                                                                                                                                                                            481 GTTATG--ACTOTITITAAACTACCTAGAAAGCCACCAGATGACATAGATGTCCACT-C 537
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/lab_host="XLI-BlueMRF'strain"
/clone lib="Bos taurus skin cDNA library"
/note="Organ: skin; Vector: Uni-ZAPXR; Site_1: EcoRI;
Site_2: Xho I; Library made from pooled skin of adult
female Hereford-Shorthorn."
                                                                                                      421 GAAAAGCTATCACGCCGAAAAGAAGTCGCCGAGTGTGTACTCCAAAAGTCAGTACGTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="Hereford Shorthorn"
/b xref="taxon:9913"
/clone="CCL003314"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  952 ATTAAACCCAAIGCTTTGATTGTTCT 977
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/organism="Bos taurus"
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Bos taurus
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BOS TEAUTUS

BOYIGAGE, METAZOGE, Chordata, Craniata, Vertebrata, Euteleostomi,

MAMMALIA: Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,

BOVIGAGE, BOVINAGE, BOS.

1. (Bases 1 to 683)

Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G.,

Wray, J.E. and Keele, J.W.

A Second Set of Bovine ESTS from pooled-tissue normalized libraries

Unpublished (2003)

Unpublished (2003)

L. Ochtact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4360

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 CTATGATTCCCTGCTGGCTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site_1: EcoR1; Site_2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
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                                                                                  CB418866 689 bp mRNA linear
291692 MARC 6BOV Bos taurus CDNA 5', mRNA sequence.
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Seg primer: GTAATACGACTCACTATAGGG.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                        CB418866
CB418866.1 GI:29183348
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                                                                                                                                                                                                                                                                                   'clone_lib="NIA Mouse Newborn Kidney cDNA Library (Long
                                                                                                                                                                                                                                                                                                                                'note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
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                                                                                                                                                               |db_xref="niaEST:B0817B10-5"
|db_xref="taxon:10090"
|clone="NIA:B0817B10 IMAGE:30469077"
                                                                                                                                                                                                                                /dev_stage="Newborn Kidney"
/lab_host="DH10B"
                                                                                          /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
High quality sequence stop: 633 POLYA=No.
                                               Location/Qualifiers
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Best Local Simil
Matches 525; C
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Placy Y. Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
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B817B10-5 NIA Mouse Newborn Kidney cDNA Library (Long 1) Mus
musculus cDNA clone NIA:B0817B10 IMAGE:30469077 5', mRNA sequence.
CF169716
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimus
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### 1707	135 GCTGGGCTGTTTCTGGTGGTTTTGTGGTGTTTGTGGTGTTTGTGGTG	120 134 ORIGIN	180 Query Match Best Local Similarity
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12 bp mRNA linear EST 10-OCT-2001
fus musculus cDNA clone IMAGE:5391109 5',
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a, Sciurognathi, Muridae, Murinae, Mus.
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Life Technologies, Inc.
The I.M.A.G.E. Consortium (LLNL)
Genomics, Inc.
Lone distribution information can be
Consortium/LLNL at:
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USDA, ARS, Beltsville Agricultural Research Center
Bd1g. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301
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University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
2024 University of Iowa
2024 University of Iowa
2024 University of Iowa
Tel: 319 356 4866
Fax: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com)
The following repetitive elements were found in this cDNA
sequence: 404-466, ART rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
                CA313163 486 bp mRNA linear EST 04-NOV-2002 UI-CF-FNO-aex-d-08-0-UI.S1 UI-CF-FNO Homo sapiens cDNA clone UCF-FNO-aex-d-08-0-UI 3', mRNA sequence.
CA313163.1 GI:24531261
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                             1 (bases 1 to 486)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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AGG TISSUB=Lung Epithelial Cells Tissue nos 359-368
TAG LIB-LT-FF-FNO
TAG_SEQ=GGCTGTAGGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 21.8%; Score 438.8; DB 14; Length 486; Best Local Similarity 99.5%; Pred. No. 1.5e-77; Matches 440; Conservative 0; Mismatches 2; Indels 0;
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Genome Res. 6 (9), 791-806 (1996)
97044477
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AUTHORS
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CA313163
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qq	182 GICCITIGAGAACTICACCIGCTCCIAIGHGHACTIGAGAAAATGICAAAATTIGT 241
ολ	1809 TCTGTGAAAATAAATTTCCTTCTTGTACCATTTCTGTTTTAGTTAAAATCTGAAA 1868
qq	242 TCTGTGAAAAATAAATTTCCTTCTTGTACCATTTCTGTTTAGTTTTACTAAAATCTGTAA 301
ζ	ADACTGIATTTTTCTGTTTATTCCAAATTTGAAGCAAACTGACAATTTGAAAGTTT 19
qq	302 ATACTGTATTTTCTGTTTATTCCAAATTTGAAACTGAAATTCCAATTTGAAAGTTT 361
δλ	1929 GIGICGACGICIGICIACTIAAAAGAAIGIGIICIAITIGGIITIATACAITIAIAAAAA 1988
qq	362 digicdakoictidictiaakidaardigirictarridetritaratarriaa 421
λõ	1989 TAAATIGTACATITICTAATT 2010
qq	422 TAAATTGTACATTTTTCTAATT 443
RESULT CF79603	24 0/c
LOCUS DEFINITION ACCESSION	CF796030 892243 MARC 4PIG Sus so CF796030
VERSION KEYWORDS	EST.
SOURCE	Sus scrota (pig) SM Sus scrota Spitarvota: Metazoa: Chordata: Craniata: Vertebrata:
0 0 0 0 0 0 0 0	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
AUTHORS	Smith.T.P.L., Freking, B.A., Ford, J.J., Val. Nohneman, D.J., Wray, J.E. and Keele, J.W.
TITE	Porcine EST collection using a normali: embryos representing early development:
COMMENT	Unpublished (2003) Contact: Smith TPL
	usda.gov Bases called with phred v0.020425.
	with the aid of the trim_alt option. Vector identifi
	Place: IMM 10 10 10 10 10 10 10 10 10 10 10 10 10
FEATURES	į
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	/mol_type="mRNA" /db_xref="taxon:9823"
	/tissue_type="pooled" /lab_host="DH10B"
	. cite 1. poobt. cite 2. NotT
	pcDNA3:1; Sice 1: ECOR1; Sice 2: th combined RNA from day-10, day- and day-30 whole embryos."
ORIGIN	
Query Best]	ry Match 21.3%; Score 429; DB 14; Length 688; Local Similarity 81.4%; Pred. No. 11.38-75; Ches 5.1; Ches 5.1; Ches 5.1; Ches 5.2; Ches 5.1; Ches 5.1; Ches 5.1; Ches 5.1; Ches 5.1; Ches 5.1; Ches 5.2; Ches 5.1; Ches 5.2; Ches 5.3; Ches 5
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// Site 2: Not1; Mouse cDNA project by the Laboratory of Site 2: Not1; Mouse cDNA project by the Laboratory of Genefics, National Institute on Aging (NIA), Intramural Research Program, WIH (http://lgsun.grc.nia.nih.gov/cDNA). Research Program, WIH (http://lgsun.grc.nia.nih.gov/cDNA). In brief, double-stranded cDNAs were synthesized with an Oligo(dT) princer Invitrogen: esynthesized with an Oligo(dT) princer Invitrogen: and programmer Invitrogen: and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the CDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were figested with Sal1 and Not1 enzymes and cloned into Sal1/Not1 site of poWV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.0 kb. The library was
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83.4%; Pred. No. 2.2e-75;
ive 0; Mismatches 97; Indels 0;
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/lab_host="DH10B"
                                organism="Mus musculus"
                                                         /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Musuryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 693)
1 (bases 1 to 693)
2 faco,Y., Ks,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
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B0808A07-5 NIA Mouse Newborn Kidney CDNA Library (Long 1) Mus musculus cDNA clone NIA:B0808A07 IMAGE:30468198 5', mRNA sequence.
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National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
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Plate: B0808 row: A column: 07
Seg primer: M13 Reverse
High quality sequence stop: 693
POLYA=No.
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Contact: Dawood B. Dudekula
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630 AGAGCTCTGTTCTGCTTTTTTTTTTTGCAACGAAAAGAGC 672 	26 8/C AA536178 1ON nEVA linear EST 21-AUG-1997 1ON NF96b03.81 NCI_CGAP_CO3 Homo sapiens cDNA clone IMAGE:927725 3', ON AA536178 I AA536178.1 GI:2280431	_	1 (bases 1 to 490) NCI-CGAP HO. 4900. NCI-CGAP TO 4900. NCI-CGAP TO 4000. National Cancer Institute, Cancer Genome Anatomy Project Tumor Gene Index Unpublished (1906) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov	ALSE FIGUREMENT: BILDS CAMEDO, M.D., MILHELT E. BURNELL-BUCK, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arraying: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.linl.gov/bbrp/image.html Insert Length: 572 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality Sequence stop: 315.	υ Φ Ο	/ Libbue_rype=rolon. / Lab host="DH10B" / clone_lib="NCI CGAP Co3" / clone=lib="NCI CGAP Co3" / note="Wetcher: pT713D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; ist strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(df) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of	/ Match 21.1%; Score 425; DB 9; Length 490; Local Similarity 100.0%; Pred. No. 8.6e-75; Gonservative 0; Mismatches 0; Indels 0; Gaps 0; 158 TTGAAGAAGAATGATTTGACAAGAAATCATATATATATGATATTTTAATAAG 1645	1646 TATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAA	1766 CCTGCTCCTATGTGGGTACCTGAGTCAAATTGTCATTTTTGTTCTGTGAAAATAAAT
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDN Library Preparation: M. Bento Soares, Ph.D.
cDN Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AJ507044 Mus musculus BALB/c (Kahlem P) Mus musculus CDNA clone 127, mRNA sequence, AJ5070444
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 752)
                                                                                                                                                                                                                                                                          CGGAGTCCAGCTGAAAACTCATCACCAGAGGATAATGGCAACCCATGGAAAATC
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         14; Length 444;
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/mol_type="mRNA"
/strain="BALB/c"
/clone="127"
/clone_lib="Mus musculus BALB/c (Kahlem P)'
                                                              Indels
tch 21.0%; Score 421.6; DB 14; al Similarity 99:1%; Pred. No. 4.2e-74; 424; Conservative 0; Mismatches 4;
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Ihnestrasse 73, D-14195 Berlin, GERMANY
Location/Qualifiers
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Mus musculus
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Best Local S:
Matches 424
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Matches 452; Conservative
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   Res.
   Genome Re
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                                                              /organism="Homo sapiens"
/mol type="mRNN"
/mol type="mRNN"
/do_xref="taxon:9606"
/clone="raxon:9602"
/clone="bream Homo
/mol type="mRNN"
/lab host="bright108"
/clone=libran: Kidney; Vector: pT7T3D-Pac (Pharmacia) with
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with
plasmid DNA from the normalized library NCT CGAP Kid3 was
prepared, and se circles were made in vitro. Pollowing HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
/clonelDs 1323376-1323911, 145607-1456775, and
150552-1502823). Subtraction by Bento Soares and M.
Patima Bonaldo.
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

Vanburen, V., Placo, Y., Dudekula, D.B., Qian, Y., Carter, M.G.,

Martin, P.R., Stagg, C.A., Bassey, U., Alba, K., Hamatani, T.,

Assembly, verification, and initial annotation of NIA 7.4K mouse

CDNA clone set
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100.0%; Pred. No. 1.4e-69;
ative 0; Mismatches 0;
Seg primer: -40UP from Gibco
High quality sequence stop: 379.
Location/Qualifiers
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CK333041.1 GI:40232656
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Best Local Simi
Matches 399;
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CK333041
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/dev attage="mixed"
/lab_host="DH10B"
/lab_host="DH10B"
/clone lib="NIA Mouse Unique Gene Set Version 2"
/note="Wetcor: pSPORT1 (Invitragen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, NotI; Mouse cDNA project by the Laboratory of Genetics, NotI; Mouse cDNA project by the Laboratory of Genetics, NotI; Mouse cDNA project on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This clone is among a rearrayed set of ll,424 clones from more than 20 cDNA libraries."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 TAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGCTCTTTCTCCCGGACCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 GAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTGGTGGTGTTGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTGGGCACAGTGGCTGTCATGCCTCAGGGAGAGTGTCGGCCTTCATTGAAAA
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              Laboratory of Generics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdne@lgsun.grc.nia.nih.gov
Plate: H8229 row: C column: 06
Seq primer: M13 Reverse
Pigh quality sequence stop: 642
POLYAANO.
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83.5%; Pred. No. 1.6e-69;
tive 0; Mismatches 89; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                         |db xref="niaEST:H8229C06-5"
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|clone="H8229C06"
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/mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                         Location/Qualifiers
Contact: Dawood B. Dudekula
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486 180 546 240 909 300

999 360 420 786 480 846 540 906 599 996 655

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AI786907 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1921700 5' similar to TR:035054 035054 CPE-RECEPTOR: ;, mRNA
                                                                           61 GCTTTCTTGGCTTTCATGACAGCCATCCTCGGAATGAAGTGCACCAGATGCACGGGGGAC 120
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., The WashU-NCI Mouse EST Project 1999
121 gardagaacereaagaeceecarcricereacaeceecaarcarcricricarcaeceec
                                                                                                                                                                                                      487 ATGGTGGTGCTCATCCCTGTGAGCTGGGTTGCCAATGCCATCACAGATTTCTATAAC
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                                      TCCTTCTTGGCTTTCATGATGGCCATGCATGAAATGCACCAGGTGCACGGGGAAC
                                                                                                                        AATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCATCATCATCACGGGC
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AI786907.1 GI:5334623
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AI786907
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Mus musculus
Mus maculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Murinae; Mus.

1 (bases 1 to 656)
Tajo,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal FCR amplification
                                                                                                                        CF168607 15-JUL-2003 MRNA linear EST 25-JUL-2003 B0802A03-5 NIA Mouse Newborn Kidney cDNA Library (Long 1) Mus musculus cDNA clone NIA:B0802A03 IMAGE:30467618 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIA Mouse Newborn Kidney cDNA Library (Long ))"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory of Genetics Mational Institutes of Health Mational Institute on Aging/Mational Institutes of Health 333 Cassell Drive, Sulte 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov Plate: B0802 row: A column: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.8%; Score 397.4; DB 14; Length 656; 77.2%; Pred No. 2.7e-69;
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/clone="N1ax 10090"
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/lab_hoste="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 11 (9), 1553-1558 (2001)
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/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Dawood B. Dudekula
                                                                                                                                                                                       CF168607
CF168607.1 GI:33278156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: M13 Reverse
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Gaps

5,

0; Mismatches 146; Indels

Conservative

Matches 510;

Similarity

Other_ESTs: uj32g11.x1 Contact: Mara M/MashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

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BI104115 ... 754 bp mRNA linear BST 26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
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/clone="IMAGE:5035638"
/tissue type="sgontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab host="nH108"
/clone lib="NHI CGAP Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
/note="Organ: clone unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NHH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226 AGTAACATTGTGGGTGTTTGAGAACCGCTGGGAAGGCTTGTGGGATGAACTGTATGAGGCAT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCATCCTCGGAATGAAGTGCACCAGATGCACGGGGGACGATGAGAACGTGAAGAGCCGC 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 GCCAACATCAGAATGCAGTGCAAGGTCTACGACTCCTGCTGGTCTTAGTCCAGACCTC 345
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                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 754)
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC.clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
polumn: 07
High quality sequence start: 2
High quality sequence stop: 653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 GGTGGGCACGGTGGCTTGTGACTATTATGCCTCAGTTGGAGAGTGTCTGCCTTCATCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 GGTGGGCACAGTGGC-TGTCACTGTCATGCCTCAG-TGGAGAGTGTCGGCCTTCATTGAA
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llarity 78.3%; Pred. No. 5.5e-68;
Conservative 0; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="Czech II"
                                                                                                                                                                                                                               Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                               BI104115.1 GI:14555008
                                                                                                                                 mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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Best Local Simil
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                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
JOURNAL
                          RESULT 33
BI104115
LOCUS
                                                                                                                                                      ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_libe="Sugano mouse kidney mkia"
//clone_libe="Sugano mouse kidney mkia"
//note="Organ: kidney; Vector: phE185-Fi3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[AIGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pME185-Fi3
vector (5' site CACTGTGTG, 3' site CACCATGTG]. XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCACA."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTGGGCACGGTGGCTGTGACTATCATGCCTCAGTGGAGTGTCTGCCTTCATCGGAAG 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372
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Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This Clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:977992
Seg primer: custom primer used
High quality sequence stop: 518.

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Pred. No. 4.1e-69;
); Mismatches 89; Indels 0
                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                           db_xref="taxon:10090"
clone="IMAGE:1921700"
                                                                                                                                                                                                                                                                                                                                                                                    dev_stage="adult"
lab_host="DH10B"
                                                                                                                                                                                                                                                          mol_type="mRNA"
strain="C57BL"
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                                                                                                                                                                                                                                                                                                                                                              'sex="female'
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Best Local Similarity 83.5
Matches 450; Conservative
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 584)
1 (bases 1 to 584)
1 Smith.T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
                                                                                                                1115
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Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
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TTTTCTAAAATGGTTCATGTTTTATTTCTTATTAGTTACTTCAAAATGACATTGTTG
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                                                                                                                                                                                                                                                                1116 GIGTAACATTTATATCTCACATA----GAGACATGCTTATATGGTTTTAAAATGAA
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/lab host="DHAIO8"
/dlone lib= DHAIO8"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                                                                                                                1056 AAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGA
                                                                                                                                                                                                                                                                                                                                      179 grónakcammengrerekennegmaganakaggernanáragreenammahangaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359 ATTTATAATGAAAGTTAAAATGGAAGCTCTAATCAGCACGGTAAATGGAACTAAATGGCT
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/organism="Bos taurus"
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/db_xref="taxon:9913"
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                                                      ATTCTGCTGACGCTGGAATCATCTTCATCACGGGCATGGTGGTGCTCATCCCTGTG 507
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/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
                                                                                                                                                                                                  AGCTGGGTTGCCATGCCATCATCAGATTTCTATAACTCAATAGTGAATGTTGCCCAA
                                                                                                                                                                                                                                                                                                                                             AAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCTGATTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAGGAGCACTGTACAGTGTGTGTCAGGTGTACTGAAAGGAGCAACCAGTTACAGGTAC
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/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="pal108"
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us-10-063-732-119.rst

found through the I.M.A.G.E. Consortium/LLNL at:

1. .918 /organism="Mus musculus"

http://image.llnl.gov Plate: LLAM8522 row: g column: High quality sequence stop: 629. Location/Qualiflers

/mol_type="mRNA"
/strain="C57Bij6d"
/db xref="taxon:10:90"
/db xref="taxon:10:90"
/clone="IMAGE:13490218"
/clone="IMAGE:13490218"
/clone="Type="tumox; gross tissue"
/dev_stage="7 months"
/lab_host="DH:0B"
/clone="Type="tumox"; Vector: pCMV-SPORT6; Site_1: SalI;
/note="Organ: mammarx"; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                           GAAACACTGATTCATTACACTGAATAAATAGAATTCAGCTATTGAGGGGAACCA
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Pred. No. 5.9e-62;
0; Mismatches 98;
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81.7%;
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AUTHORS
TITLE
JOURNAL
COMMENT
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BE285566
                                                       ORIGIN
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                                                                                                                                                                                134 GGTGGGCACGGTGGCTGTGACTATCATGCCTCAGTGGAGAGTGTCTGCCTTCATCGAAAG 193
                                                                                                                                                                                                                   269
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                                                                                                                                                                                                                                                                                          270 TAAC-ATCAGGATGCAGTG-CAAAATCTATGATTCCCTGCTGGTCTTTCTCCCGGACCTA 327
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                                                                         GAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTGGTGGTGTTGGAAT
                                                                                                         GGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGAGTGTCGGCCTTCATTGAAAA
                                                                                                                                                                                                                   194 TAACATTGTGGTGTTTGAGAACCGCTGGGAAGGCTTGTGGATGAATTGTATGAGGCATGC
                                                                                                                                                                                                                                                                                                                                                                 CAGGCAGCCAGAGCACTGATGTGTGCTGCTTCCGTGATGTCCTTCTTGGCTTTTCATGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           554 AAAGCGTGAGCTGGGAGAAGC-CTCTACATAGGCTGGACCACAGGCGCT-GTGCTGATCGC
                                    Gaps
                                  .,
918;
 Length
                                  Indels
17.9%; Score 360.4; DB 10;
83.0%; Pred. No. 6.5e-62;
iive 0; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     767 bp
AGENCOURT 11444483 NIH MGC 166 Mus
IMAGE:30246099 5', mRNA sequence.
CB235084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGAGGAGCTCTGTTCTGCTGCGTTT 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGATGAGCCCTGTTCTGTGGTGTGT
                                    Conservative
                   Best Local Similarity
Matches 470; Conserv
                                                                                                                                                                                                                   210
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 Query Match
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CB235084
LOCUS
DEFINITION
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Email: cgapbs-r@mail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be

```
/organism="Homo sapiens"
/mol type="mRNA"
/db Xref="taxon.9606"
/db Aref="taxon.9606"
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/db host="Pill0B (TI phage-resistant)"
/db host="Pill0B (TI phage-resistant)"
/dlone lib="NIH MGC 75"
/note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site_I:
/note="organ: Kidney; Vector: plangerategoch; Site_I:
/note="organ: Kidney; Vector: plangerate and vector organ: Vector organ; Vector organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX283446 BX BX283446 NIH MGC_75 Homo sapiens cDNA clone IMAGP958G091346 ; IMAGE:4606880, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo saplens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 355)

Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.

Unpublished (2003)
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                   509 GCTGGGTTGCCANTGCCANCATCATCAGATTTCTANACTCGATGATGTTGCCCAAA
                                                           607 GCTGGGTTGCCAATTCCATCAGAGACTTCTACAACCCACTGGTGGATGTGGCCCCTA
                                                                                                                                                                                                                                      667 AAGCGCGAGCTGGGGGAAGCCCTCTACATAGGCTGGACCACAGCCGCTGGTGCTGATCG
                                                                                                                                                                      569 AACGTGAGCTT--GGAGAAGCTCTCTACTTAGGATGGACCAC-GGCACTGGTGCTGATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Ina Rolfs
Rapp Deutsches Ressourcenzentrum fuer Genomforschung Gmb
Rapp Deutsches Ressourcenzentrum fuer Genomforschung Gmb
Rapp: Ina Neuenheimer Feld 580, D-69120 Heidelberg, Germany
Rapp: InAGp9586091346.
RappLils; I.M.A.G.E. CDNA Clone Collection;
RappLils; I.M.A.G.E. CDNA Clone Collection;
Human UnigeneSet - Rapp3 (RappLils No.972)
http://www.rapd.de/CloneCards/cgi-
bin/showLib.pl.cgi/respons@?libNo=972 Contact: Ina Rolfs
Rapp Deutsches Ressourcenzentrum fuer Genomforschung Gmb;
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
Fax: rapd.de
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Best Local Simil
Matches 355; C
                                                                                                                                                                                                                                                                                                                                                                                                     727
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
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BX283446
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AUTHORS
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JOURNAL
COMMENT
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/mol_type="mark"
/mol_type="mark"
/dobe="mark"
/lab_host="mark"
/lab_host=
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                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 751)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATCCTCGGAATGAAGTGCACCAGATGCACGGGGGACGATGAGAACGTGAAGAGCCGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs_remail.nih.gov
Tissue procurement: T. Rajendra Kumar and Martin M. Matzuk
Tissue Procurement: T. Rajendra Kumar and Martin M. Matzuk
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCMO2 row: k column: 04
High quality sequence stop: 524.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .767
/organism="Mus musculus"
                                                                       Mus musculus (house mouse)
GI:28286662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 446; Conservative
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                                                                                                                   Mus musculus
   CB235084.1
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ö 84 25 ACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGGAGTCCAGCTGGCTAAAACTCA Gaps . 0 Length 355; Indels ö 17.7%; Score 355; DB 13; 100.0%; Pred. No. 9.6e-61; tive 0; Mismatches 0;

tissue mRNA and cDNA amp low stringency condition	Query Match 17.5%; Score 351; Best Local Similarity 98.6%; Pred. No. 6 Matches 354; Conservative 0; Mismatch Qy 1082 TTTCTCCACGACATAGCATTATGTACATAGA	Db 1 TTCTACAGGCAFAGCATTATGTACAFAGA OY 1142 ACATGCTTATATGGTTTTAAAATGAAA	Db 61 ACATGCTTATATGGTTTTATTTAAAATGAAA Qy 1202 CTCAACTATTGCTTTTCAGGGAAATCATGGA	121	13.2	RESULT 40 BE000282 LOCUS LOCUS BE000282 BE000282 BE000282 ACCESTON BE000282.1 GI:8260515		EMARYOLAS Medazoa; Unordata; Ura Mammalia; Eutheria; Primates; Cat 1 (bases 1 to 352) AUTHORS Dias Neto, B., Gancia Correa,R., V Nagai,M.A., da Silva,W. Ur., Zago Goldman,G.H., Carvalho,A.F., Mats Brunstein,A., Gollvaira,P.S., Bu	Simpson, A.J. TITLE Shocgun sequencing of the human t sequence tags JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 MEDLINE 20202663 PUBMED 10737800 COMMENT CONTACT: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Resea Rua Prof. Antonio Prudente 109, 4 Brazil Brazil	FEATURES FEATURES FEATURES FEATURES FEATURES FEATURES FINDS FINDS FINDS FOR THIS SEQUENCE WAS GETIVED FORM THE FORDS FOR THIS SEQUENCE WAS GETIVED FOR FOR THE FOR THE SEQUENCE FOR FOR THE FOR THE SEQUENCE FOR THE FEATURES FEATURES FEATURES FEATURES FOR FINDS FOR FINDS FEATURES FEATURES FOR FINDS
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Verjovski-Almeida, S., Briones, M.R., go.M.A., Bordin, S., Costa, F.F., rsukuma, A., Bala, G.S., Simpson, D.H., Buther, P., Jongeneel, C.V., l.R.R., Reis, L.F., de Souza, S.J. and
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Homo sapiens cDNA, mRNA sequence.
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/note="Organ: breast normal; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUCl8 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions.
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(Dases 1 to 351)

Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Burnsteini, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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Pred. No. 3.5e-59;
0; Mismatches 3; Indels 0;
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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BE814313.1 GI:10246547
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Best Local Similarity 99.1%;
Matches 349; Conservative (
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Fax: +55-11-2707001
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/do rate="axon.9606"
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/sote="organ: breast normal; Vector: pucl8; Site_1: Smal;
/sote="organ: breast normal; Vector: pucl8; Site_1: Smal;
/sote from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUCl8 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under
low stringency conditions."
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Froject. This proper as seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmil.pl?tl=&t2=MR0-BN0070-270
500-026-e03&t3=2000-05-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 351.
Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

( Dases 1 to 596)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Sasaki, T., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1331 TGTAAAGGAAATTGAATGGCTTTCTGATATGCTGTTTTTTAGCCTAGGAGTTAGAAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTAAAAGGAAATTGAATGGCTTTCTGATATGCTGTTTTTTTAGCCTAGGAGTTAGAAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACATAGCATTATGTACATAGATGAGTGTAACATTTATATCTCACATAGAGACATGCTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1211 TGCTTTTCAGGGAAATCATGGATAGGGTTGAAGAAGGTTACTATTAATTGTTTAAAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.2%; Score 345.2; DB 10;
99.1%; Pred. No. 8.8e-59;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                    sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                        /organism="Homo
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BB618773.1 GI:16458253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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Contract: Totaliniane mayabilization Research Group, RIKEN Genomic Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-92
Fax: 81-45-503-922
Fax: 81-45-503-92
Fax: 81-45-5 was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI." /clone lib=RREN full-length enriched, 8 days embryo"
/clone lib=RREN full-length enriched, 8 days embryo"
/note="Site 1: Sal1; Site 2: BamH1; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTVN 3'], cDNA was Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details. Gaps 0; 16.9%; Score 339.8; DB 10; Length 596; 84.2%; Pred. No. 9.5e-58; ive 0; Mismatches 72; Indels 0; et al. 2001) 'dev stage="8 days embryo" |lab_host="DH108" organism="Mus musculus" /db_xref="taxon:10090" /clone="5730424M09" Mouse ESTs (Arakawa, T., Contact: Yoshihide Hayashizaki Location/Qualifiers /mol_type="mRNA" /strain="C57BL/6J" 383; Conservative tissues. Local Similarity e monse 90 Query Match Best Loca Matches TITLE JOURNAL COMMENT FEATURES ORIGIN à

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GAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTGGTGGTGTTGGAAT 149 GAGGACGATGGCAACCTACGCTCTTCAATGGCTGCACTGGTGCTTGGTGGTGTTGGCAT 201 142

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mocray LaD
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mocray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this CDNA
sequence: 1-58, AI rich#Low_complexity (matched compliment) CB306981
UI-CF-FN0-aen-j-20-0-UI.sl UI-CF-FN0 Homo sapiens cDNA clone
UI-CF-FN0-aen-j-20-0-UI 3', mRNA sequence. 329 269 321 381 389 441 449 501 509 561 Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 363) Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene 450 TCTGCTGACGGCTGGAATCATCTTCATCATCAGGGCATGGTGGTGGTCATCCCTGTGAG 262 TAACATTGTGGTGTTTGAGAACCGCTGGGAAGGCTTGTGGATGAATTGTATGAGCCATGC caacarcagaargcagrecaagreracaacrecerecreererragrearecagaeereea CATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACAT 442 carcercegaargaagrecaccagarecaegegegegegegagaagaagaagaagagegear GGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGAGTGTCGGCCTTCATTGAAAA 330 GGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTCTTGGCTTTCATGATGGC 382 GGCATCCCGAGGACTGATGTGTGCTGCGTCCTTGGCTTTCTTGGCTTTCATGACAGC 510 CIGGGTTGCCAATGCCATCAGAGATTTCTATA 544 CTGGGTTGCCAATTCCATCACAGAGACTTCTACA 596 /mol_type="mRNA" /db_xref="taxon:9606" /clone="UI-CF-FN0-aen-j-20-0-UI" Genome Res. 6 (9), 791-806 (1996) 97044477 organism="Homo sapiens" location/Qualifiers CB306981.1 GI:28847492 Homo sapiens (human) Contact: McCray, PB McCray Lab discovery 8889548 202 210 322 390 150 562 CB306981/c LOCUS DEFINITION source VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE MEDLINE . PUBMED COMMENT ACCESSION RESULT 43 JOURNAL FEATURES 8 g ઠે 엄 ç g ò d ò g ò g ò

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/est stage="pool of ventral and dorsolateral prostate"
/dev stage="adilt, 10 week"
/lab_host="bH108 (Tl phage-resistant)"
/clone_lib="NOI CGAP_BT51"
/note="Organ: prostate; Vector: pCWV-SPORT6.1; Site_1:
Not; Site_2: BcoRV, Cloned unidirectionally. Primer:
Noligo dT. Pool of 2 primary libraries: NCI CGAP_BT46
(ventral prostate from 10 wk male, average insert size 2 kb) and NCI_CGAP_PT47 (dorsolateral prostate from 10 wk male, average insert size 2 kb) and NCI_CGAP_PT47 (dorsolateral prostate from 10 wk male, average insert size 2 kb). Constructed by Invitrogen. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI048929 465 bp mRNA linear EST 08-JUL-1998 uc84g08.yl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1432382 5' similar to TR:035054 035054 CPE-RECEPTOR: ', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.5%; Score 332.4; DB 14; Length 568; llarity 79.5%; Pred. No. 2.9e-56; Conservative 0; Mismatches 103; Indels 1;
Seg primer: M13RP1 reverse primer (ABI)
Location/Qualifiers
1. 568
/organism="Rattus norvegicus"
/mol type="mRNA"
/db xref="t-axon:10116"
/clone="IMAGE:5621868"
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                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 404;
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KEYWORDS
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AI048929
LOCUS
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/tissue_type="Human Lung Bpithelial cells"
/lab host="Mills" Life Technologies) (T1 phage resistant)"
/clone_lib="U1-CF-ND."
/clone_lib="U1-CF-ND."
/note="Crgan: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1; U1-CF-ND is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1995. For additional information, contact:
Dento-scare@ulowa.edu
TAG_ISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG_LIB=U1-CF-FNO
TAG_ESQ=GGCTGTAGGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs remail.nib.gov

CDNA Library Preparation:

CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC)

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAATTIGAAAGITIGIGICGACGICTGTCIAGCTIAAAIGAATGIGITCIAITTGCITTA 1974
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 568)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 ACTAAAATCTGTAAATACTGTATTTTTTTTTTTTTTTCCAAATTTGATGAAACTGACAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA339169 S68 bp mRNA linear EST 04.
NISC_lx11e07.y1 NCI_CGAP_Pr51 Rattus norvegicus cDNA clone
IMAGE:5621868 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                     Query Match
16.7%; Score 336; DB 14; Length 363;
Best Local Similarity 100.0%; Pred. No. 6.1e-57;
Matches 336; Conservative 0; Mismatches 0; Indels 0
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Norway rat)
Rattus norvegicus
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AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., AUTHORS Marra, M., Hillier, L., Lacy, M., Le, M., Martin, J., Morris, M., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,	Oy Qu	463 GGAATCATCTTCATC! 361 GGAATCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTC
TITLE The Washu-HHMI Mouse EST Project COMMENT Contact: Marra M/Nouse EST Project COMMENT Contact: Marra M/Nouse EST Project	y do	523 GCCATCATCAGAGAT
Mashio-naul Mouse Esi Figlet. Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810	RESULT 46 AI547146 LOCUS DEFINITION	AIS47146 PN3.1_01_G02.r my
Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.	ACCESSION VERSION KEYWORDS	A1547146 A1547146.1 GI:440 EST. Homo gabiens (hum
NGL:910:90 Seq primer: custom primer used High quality sequence stop: 457. FEATURES	ORGANISM	Homo sapiens Eukaryota; Metazo
source 1465 /organism="Mus musculus" /mol t-vne="mpNa"	REFERENCE AUTHORS	<pre>1 (bases 1 to 77 Huang, G.M., Ng, W. and Hood, L.</pre>
/strain="057BL" /db_xref="taxon:10090" /clone="IMAGE:1432382"	TITLE JOURNAL MEDLINE	Prostate cancer e. Genomics 59 (2), 99339982
/sex="female" /dev stage="adult" /lbb.bcap="adult"	COMMENT	10409429 Contact: Guyang M. Lerov Hood
/lad_nosper_Data on mouse kidney mkia" /clone lib="Sugano mouse kidney mkia" /clone lib="Sugano mouse kidney mkia" /clone lib="Sugano was kidney; Vector: pME18S-Fi3; Site 1: DraIII (CACTGTGTG); Site 2: DraIII (CACTGTGT); lst strand cDNA was primed with an oligoidT) primer [ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-Fi3 vector (S' site CACTGTGT, 3' site CACCATGTG). XhoI should be used to isolate the CDNA insert. Size selection was performed to exclude fragments -1.Skb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: S' end primer CTTCTGCTCTAAAAACTGGG and 3' end primer CTAACTGTAACACACAA.	FEATURES SOUYCE	
ORIGIN PATIENT CONCURS CONCURS OF THE CONTROL OF TH		(Stratag prostate
Length 465;	ORIGIN	
, AC	Query Match Best Local Matches 49	tcn al Similarity 70. 497; Conservative
Db 1 ACCTACGCTCTTCAAATGGCTGCTCTGGTGGTGGTGGTGGTGGTGGGCGTTG 60	ζ٥	781 ATGTTTTTTAACTT
Qy 163 GCTGTCACTGTCATGCCTCAGTGGAGAGTGTCGCCCTTCATTGAAAACATCGTGGTT 222	qu	13 AGGITTITINAACII
Db 61 TCTGTTTCTATCATGCCTCAGTGCACAGCGTCTCCTTCATCGAAAGTAACATTGTGGTG 120	δō	841 AAATGGACCCCAAAG
Qy 223 TTTGAAAACTTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGC	අ _ධ	73 AAATGGACCCAAAG
OY 283 CAGIGCAAAATCTAIGATICCCIGCIGCICCTITCICCGGACCTACAGGCAGCCAGAGA 342	ΩD	133 ACTGTGCATCAGCTA
CAGTGCAAGGTCTACGACTCCCTGCTGGCTCTTAGTCCAGACTCCAGGGATCCCGAGGA	٥, و	961 AATGCTTTGATTGTT
Oy 343 CTGATGTGGGGGGGTTCCGTGATGTCTTCTGGCTTTCATGATGGCCATCCTTGGCATG 402 Db 241 CTGATGTGCTGCTGCTCTTGGCTTTCATGATGATGATGATGATGCATCCTCGGAATG 300		193 AATGCTTTGATTGTN 1021 CTCTTTTTATCATTT
403 AAAIGCACCAGGIGCACGGGGGACAAIGAGAAGGIGAAGGCTCACAIICIGCIGACGGCI	_ qa	253 CTCTTTINATCATTT

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771 bp mRNA linear EST 09-AUG-1999
ynorm Homo sapiens cDNA 5', mRNA sequence.
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                                               CATCACGGGGATGGTGGTCCTCCCTGTGAGGTGGGTTGCCAAT 522
CACGGGGGACGATGAGAACGTGAAGAGCCGCATCTTGCTGACAGCC 360
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pe="mRNA"

if="taxon:9606"

lib="taxon:9606"

forgan: Prostate; Vector: pBluescript; Directional
ibrary was constructed using Lambda ZP II kit
ibrary was extracted from a frozen normal
et issue (Mayo Clinic)."
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ia, Primates, Catarrhini, Hominidae, Homo.
71)
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lecular Biotechnology, Box 357730, University of
:tle, WA 98195
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0.9%; Pred. No. 1.9e-55;
7e 0; Mismatches 162; Indels 42; Gaps
                                                                                                                     TITCTATAACTCAATAGTGAATGTTGCCCAA 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matthew Huang
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n/Qualifiers
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Fri Sep

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y. Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. Location/Qualifiers Location/Qualifiers Location/Qualifiers Lofd xref="texon:10090" Abore="texon:10090" Abore="texon:10090" Abore="anale" Alab_host="source" Abore="source tissues" Abore="source tissues"	Cantributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5.] GAGAGAGAGAGACTCATATATATATATATYN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5.] and the primer adapter of sequence [5.] cDNA was cleaved with XhoI and Sstl. " Query Match 16.2%; Score 325.2; DB 10; Length 643; Best Local Similarity 70.4%; Pred. No. 7.8e-55; Matches 435; Conservative 0; Mismatches 183; Indels 0; Gaps 0;	QY 90 GAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGCTGTTTCTTGGTGTGTTGGAAT 149 Db 25 GAGGACAATGGGAACCTACTAGAATGGCTGCACTGGTGTTTCTTGGTGTTGGAAT 84 QY 150 GGTGGGACAGTGGCTGTCACTGTCATGCTAGTGGAGGTGTCGGCGTTGGAAT 209 BS [Db 205 CANCHIGAGAATGCATTGCAGGACTTCCTCTTTTTTTTTTTTTTT
1081 ATTCTCCAC-GACATAGGATTATGTACATAGATGAGTGTAACATTTATATCTCCACATAG 1139 313 ATTCTCCAC-GACATAGGATTATGTACATAGATGAGTGAACATTTATTATTATTATTATTATTATTATTATTATTATT	RESULT 47 BB610589 LOCUS BB610589 LOCUS DEFINITION BB610589 RIKEN full-length enriched, adult male tongue Mus musculus cDKA clone 2310031C15 5', mRNA sequence. ACCESSION BB610589. I GI:16452086 KEYWORDS EST. ORGANISM Mus musculus (house mouse) ORGANISM Mus musculus (house mouse) CRGANISM CRGANISM Musculus (house mouse) CRGANISM CRGANI	Arak Harak Obono Sogno Take Unpur Cont Cont 1-7-	Tell 81.45-503-9212 Fax: 81-45-503-9212 Fax: 81-45-503-9212 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp, Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res0 (100), 1617-1630 (2000) wagi,K., Fujiwake,S., Inouce,K., Togawa,Y., Izawa,M., Ohara,E., Matauixa,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer. Genome Res 10 (11), 1757-1771 (2000)

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.,Y., Shibata,K., Itoh,M., Carninci,P.,
Ishizaki,Y.
Jods for the mouse full-length cDNA
ime sequence clustering for construction of sbrary. Genome Res. 11 (2), 281-289 (2001)
LA., Saito,T., Kiyosawa,H., Yamanaka,I.,
Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                            sis of Full-Length Mouse cDNAs Compared with es. Mamm. Genome. 12, 673-677 (2001) b site (http://genome.gsc.riken.go.jp) for
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Pred. No. 7.8e-55;
0; Mismatches 183; Indels 0;
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="adult"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
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/dev_stage="7 months"
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/note="Organ: māmmary; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally, Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
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Nort-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                             181 AGGAGCTCTGTTCTGCTGCGTTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACAGATACTC
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81.0%; Pred. No: 9.7e-54;
tive 0; Mismatches 87; Indels 0;
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/db_xref="taxon:10090"
/clone="IMAGE:3669054"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamalia; Eutheria; Primates; Catarrhin; Hominidae; Pan.
1 (bases 1 to 325)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Fodd, W.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA.
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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                                          GTGGGGTGCCTATTCCATCATCAGAACTTCTAGAACCCACTGGCGGATATGGTCCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGCTCATCCCTGTGAG
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Pred. No. 2.1e-54;
0; Mismatches 1;
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/db_xref="taxon:9598"
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99.7%; Pred
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gene="CLDN8"
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Query Match 15.5%; Score 311.2; DB 9; Length 348; Query Match Best Local Similarity 99.1%; Pred. No. 5.7e-52; Matches 313; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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1031 CATTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAATTTCTCCAC 1090

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348 bp mRNA linear EST 08-FEB-1998
020c04:s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324230 3',
MRNA sequence.
                     239 TAACATIGIGGIGITIGAGAACCGCTGGGAAGGCTIGIGGAIGAATIGIATATGAGCAIGC 298
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299 caacarcaaaargcagracaagrichacdacriccrigcriggrichragriccagaccricca 358
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                                                                                                                                                                                                                      CATCCTCGGAATGGAGTGCACCAGATGCACCGGGGACAATGAGAACGTGAAGAGCCGCAT
                                                                                                                                                                                                 CATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACAT
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                                                                TAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCT
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: Cagabs-remail.nih.gov
unknown library type
Insert Length: 1460 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 223.
Location/Qualifiers
1. .348
//cganism="Homo, sapiens"
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Homo sapiens
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                                                                                                                                                                                                                                                                                  1271 GCTTAGGGATTAATGTCCTCCATTATAATGAAGATTAAAATGAAGGCTTTAATCAGCGT 1330
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348 CATITACTICAAAAIGACATIGCIAAAGACIGCAITATITIACIACIGIAAITICICCAC 289
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                                                                                              288 GACATAGCATTATGTACATAGATGAGTGTAACATTTATATCTCTCACATAGAGACATGCTTA
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                                                             1091 GACATAGCATTATGTACATAGATGAGTGTAACATTTATATCTCCACATAGAGACATGCTTA
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Search completed: September 3, 2004, 00:56:25 Job time : 3563 secs

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BCC20866 Homo sapi
AA250711 Homo sapi
AX09238 Sequence
AX09729 Sequence
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AX131927 Homo sapi
AC131927 Homo sapi
AC131927 Homo sapi
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1 MATHALEIAGLFLGGVGMVG......QKSYHTGKKSPSVYSRSQYV 225
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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(bases) Lo 1700)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shennen, C.M., Schuler, G.D.,
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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecton, M., Scares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Rana, S.S., Loquellano, N.A., Peters, G.J.,
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Fahey, J., Helton, E., Ketteman, M., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerzhield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002)
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Contact: MGC help desk
Contact: MGC help desk
Contact: MGC help desk
Contact: MGC help desk
Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaichersburg, Maryland;
Web Sate: http://www.nisc.nih.gov/
Contact: nisc mgc@mycmin.nisc.nih.gov/
Contact: nisc mgc@mycmin.sc.nih.gov/
Contact: nisc mgc@mycmin.sc.nih.gov/
Contact: N. Ayele, K. Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakeley, R.W., Bouifard, G.G., Breen, K., Brintley, C., Haphighi, P.,
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Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 48 Row: d Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21314655.
Location/Qualifiers
     всирвиод
Homo sapiens claudin 8, mRNA (cDNA clone MGC:61830 IMAGE:4606880),
complete cds.
                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Straubberg, R.
Direct Submission
Bubmitted (18-SEP-2003) National Institutes of Health, Mammalian
Submitted (18-SEP-2003), Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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AUTHORS
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201 SerHisargThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer 	221 ArgserGlnTyrVal 225 	BCO20866 Homo sapiens claudin 8, mRNA complete cds. BCO20866 BCO20866 BCO20866 BCO20866 BCO20866 BCC20866 BCC20866 BCC20866 BCC20866 BCC20866 BCC20866 BCC20866 BCC20866 BCC20866 BCC2086 BCC2086 BCC2086 BCC2086 BCC2086 BCC208 B
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GlyMetlysCysThrArgCysThrGlyAspAsnGluLysVallysAlaHisIleLeuLeu 120
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 36 Row: e Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21314655.

1. 1835

/organism="Homo sapiens"

FEATURES

	1931 bp DNA linear PRI 11-NOV-1999 QY 101 1:6433859 NN8 gene for claudin-8. Chaman) Lazoa; Chordata; Catarrhini; Hominidae; Homo. Inglehearn, C.F. Ing	QY 201 SerHishrgThrThrGlnLySSerTyrHisThrGlyLySLySSerProSe Db 623 TCCCATGGCACAACCCAAAAAGTTATCACACCGGAAAGAAGTCACCGAA QY 221 ArgSerGlnTyrVal 225 Db 683 AGAAGTCACTATGTG 697 RESULT 4 AX092388 2010 bp DNA linear AX092388 LOCUS AX092388 AX092388 linear linear PEFINITION Sequence 119 from Patent WO0116318. LOCUS AX092388 locus linear ACCESSION AX092388 GI:13444508 KEYWORDS KEYWORDS Homo sapiens (human) REFERENCE Homo sapiens (human) Relation with the sapiens Craniata; Vertebrata; POKSYHTGKKSPSV REFERRINCE Hominidae; Putheria; Primates; Catarrhini; Hominidae; Ritheria; Primates; Catarrhini; Hominid	.5e-123 Length: 1931 172.00 Matches: 225 00.00% Conservative: 0 00.00% Mismatches: 0 00.00% Indels: 0 00.00% Gaps: 0 x HSA250711 (1-1931) x HSA250711 (1-1931) A110111111111111111111111111111111111
10 10 10 70	L GELSE S AS L		ORIGIN Alignment Scores: 6.5e-123 Length: Pred. No.: 5Core: 1172.00 Matches Percent Similarity: 100.00\$ Mismatc Ouery Match: 100.00\$ Indels: 09 Gaps: US-10-063-732-120 (1-225) x HSA250711 (1-1931) Oy

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δy	1 MetAlaThrHisAlaLeuGluIl	eAlaGlyL	euPheLeuGlyGlyValGl	yMetValGly 20 	Alignmer
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δλ	21 ThrvalAlaValThrvalMetProGlnTrpArgValSerAlaPhelleGluAsnAsnIl	ProGlnTrpArgValSez	AlaPheileGl	luAsnAsnIle 40	Percent
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γ̈́ο	41 ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCy	GluGlyLeuTrpMetAsr	CysValArgGlnAl	InAlaAsnIle 60	, co
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ζŏ	61 ArgMetGlnCysLyslleTyrAspSerLeuL	AspSerLeuLeuAlaLeu	euAlaLeuSerProAspLeuGlnAlaAl	euGlnAlaAla 80	÷ ÷
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δλ	81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetMetAlaIleLeu	SerValMetSerPhele	AlaPheMetMe	stAlaIleLeu 100	
Db 3	337 AGAGGACTGATGTGTGCTTCCGTGATGTCCTTCTTGGCTTTCATGATGGCCATCCT	TCCGTGATGTCCTTCTTC	GCTTTCATGAT		g ;
27 1	101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu	ThrGlyAspAsnGluLys	ValLysAlaHi	SI]eLeuLeu 120	<u> </u>
Db 3	397 GGCATGAAATGCACCAGGTGCACGGGGACAATGAGAAGGTGAAGGCTCACATTTTTGCTG	ACGGGGACAATGAGAAG	GTGAAGGCTCA	ACATTCTGCTG 456	8 8
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Qy 1	141 AlaasnalaileileargaspPheTyrasnSerileValasnValalaGlnLy	PheTyrAsnSerIleVal	AsnvalAlaGl		7 20
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Qy 1	161 LeuGlyGluAlaLeuTyrLeuGlyTrpThrThrAlaLeuValLeuIleValGlyGlyAl	GlyTrpThrThrAlaLeu	ValleulleVa	alGlyGlyAla 180	- F
Dp 2	577 CTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCTGATTGTTGGAGGAGCT	GGATGGACCACGGCACTC	GTGCTGATTGT	rrecaecaecr 636	8 8
Oy 1	181 LeuPheCysCysValPheCysCy	CysAsnGluLysSerSerSer	SerTyrArgTy	/rSerIlePro 200	Z dd
9 qa	637 crgrrcrgcrgcrrrrrrrrgracaaaaaaaaaaaaaaa	TGCAACGAAAAGAGCAGT	AGCTACAGATA	Acredaracer 696	8
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9 qa	697 TCCCATCGCACAACCCAAAAAAGTTAT	AGTTATCACACCGGAAAGAAGT	aagtcacccac	scerciacice 756	8
Qy 2	221 ArgSerGlnTyrVal 225				G 6
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RESULT 5 AX376290					
LOCUS	AX376290 Sequence 357 from Patent	2010 bp DNA t WO0168848.	linear	PAT 01-MAR-2002	λō
VERSION	AX376290.1 GI:19170536				qq
SOURCE	Homo sapiens (human)				ŏ
ORGENT OF	nomo sapiens Eukarvota: Metazoa: Chordata: Craniata: Vertebrata:	rdata: Craniata: V	ertebrata:	Euteleostomi:	qu

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Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
Janang,Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
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Patent: WO 016848-A 357 20-SEP-2001;
Genentech, Inc. (US)
Location/Qualifiers

Homo sapiens (human). Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE AUTHORS

JOURNAL TITLE

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Enkaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. (bases i to 2010)

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Effort to Identify Novel Human Secreted and Transmembrane Proteins:
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Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
Location/Qualifiers
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Genome Res. 13 (10), 2265-2270 (2003)
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TITLE JOURNAL COMMENT Dinguistics of the series of t ACLILYZ7
HOMO SADJENS Chromosome 8 clone RP11-945D10 map 8, LOW-PASS
SEQUENCE SAMPLING. 140 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheMetAlaIleLeu 100 120 397 GGCATGAAATGCACCAGGTGCACGGGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTG 456 141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160 LeuGlyGluAlaLeuTyrLeuGlyTrpThrThrAlaLeuValLeuIleValGlyAla 180 636 200 CIGITCIGCIGCGITITITIGITGCAACGAAAGAGCAGTAGCTACAGATACTCGATACCT 696 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer 220 TCCCATCGCACAAACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCGTCTACTCC 756 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 81583)
Birren, B., Nusbaum, C. and Lander, E. Homo sapiens chromosome 8, clone RP11-945D10 577 CTTGGAGAAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCTGATTGTTGGAGGAGCT LeuPheCysCysValPheCysCysAsnGluLysSerSerSerTyrArgTyrSerIlePro 277 AGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTTTCTCCGGACCTACAGGAGCCC 337 AGAGGACTGATGTGTGTGCTGTGTGTGTCCTTCTTGGCTTTCATGATGGCCATCCTT GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu GCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAATGTTGCCCAAAAACGTGAG 61 ArgMetGlnCysLysIleTyrAspSerLeuLeuAlaLeuSerProAspLeuGlnAlaAla AC131927 AC131927.2 GI:27414257 HTG; HTGS_PHASE0. HOMO SADiens (human) Homo sapiens 221 ArgSerGlnTyrVal 225 757 AGAAGTCAGTATGTG 771 637 517 161 181 201 697 101 RESULT 8 AC131927/c VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS ACCESSION ò δ a δ Db g δ 셤 gg à g ò 윱 ò g g $\dot{\delta}$ ò

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Db 35900 CTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGACCAGTAGCTACAGATACTCGATACCT 35841 Qy 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysSerProSerValTyrSer 220	AP000884/c LOCUS AP000884 LOCUS DEFINITION Home sapiens genomic DNA, chromosome 21q22.1, clone:B463d19, DEFINITION SOD-AML region, complete sequence. ACCESSION AP000884 VERSION AP000884.1 GI:6580113 KEYWORDS HTG. SOURCE Home sapiens (human)	CKGENISM Town Saging and Action of the Craniata, Vertebrata; Buteleostomi, Bukaryota, Memalia, Butheria, Primates, Catarrhini, Hominidae, Homo. REFERENCE 1 (bases 1 to 137955) AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. TITLE Homo sapiens 137, 955 genomic DNA of 21q22.1 JOHENAL Published Only in DataBase (1999)	AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Secg, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. TITLE Direct Submission JOURNAL Submitted (15-DBC-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-855, Japan (B-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924) PEATURES Location/Qualifiers	<pre>source 1137955 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="21" /map="21q22.1" /clone="8463J19"</pre>	Alignment Scores: 1.42e-120 Length: 137955 Score: 1172.00 Matches: 225 Score: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 9 Gaps: 0 US-10-063-732-120 (1-225) x AP000884 (1-137955)	MetalaThrHishlaLeuGlullealaGlyLeuPheLeuGlyGlyWalGlyMetValGly 20

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              Varso, M.L.

Direct Submission

Direct Submission

L Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular Genetics (addresses see below)

On Jan 16, 2002 this sequence version replaced gi:7717317.

The chromosome 21 mapping and sequencing consortium consisting of * RIKEN Genomic Sciences Center, Human Genome Research Group, * e.mail: hattori@gsc.riken.go.jp

* e.mail: hattori@gsc.riken.go.jp/
Gardiner, K., Nizetic, D., Francis, F., Lehrach, H., Reinhardt, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Keio University School of Medicine, Molecular Biology, * Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * GBF, Dept. of Genome Analysis,
* Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
info.genome@gbf.de
* URL: http://genome.gbf.de/
                                                                                                                                                                                                                                                                                                                                                                 * Institute of Molecular Biotechnology, Genome Analysis, *
Bettenbergstrasse 11, D-0715, Jena, Germany,
* e.mail: gscj-submit@genome.imb-jena.de
* URL: http://genome.imb-jena.de/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * Max-Planck Institute for Molecular Genetics,
* Ihnestrasse 73, D-14195 Berlin, Germany,
* e.mail: info-chrzlemolgen.mpg.de
* URL: http://chrzl.rz-berlin.mpg.de/
AL163252: Submitted (10-Apr-2000).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="P681K20, 5' partial"
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/clone lib="RPCI-11 BAC library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160-8582, Japan,
* e.mail: nshimizu@dmb-med.keio.ac.jp
* URL: http://www.dmb.med.keio.ac.jp/

    48622
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Unaces 1 to 176580)
User Cai,Z., Wang,B., Zheng,H., Zhang,Y., Zhang,X., Zhu,G.,
Uu,G., Fu,G. and Chen,Z.
Uu,G., Fu,G. and Chen,Z.
Unitted (26-MAY-2003) Shengyue Wang, Chinese National Human
Genome Center at Shanghai, Genomic Sequencing; No.250 BiBo Road,
Genome Center at Shanghai, Genomic Sequencing; No.250 BiBo Road,
Genomic Center at Shanghai, MELINETP://www.chgc.sh.cn,
The Chinasyechgc.sh.cn, URL:http://www.chgc.sh.cn,
The Chinase Chromosome 22 Sequencing Consortium consists of:
The Chinase National Human Genome Center at Shanghai, Shanghai, China;
GEBF, Dept. of Genome Analysis, Braunschweig, Germany; *Institute
of Molecular Biotechnology, Jena, Germany; *KRIBB Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://chgc.sh.cn

Contact: wangsy@chgc.sh.cn

Contact: wangsy@chgc.sh.cn

Contect: wangsy@chgc.sh.cn

Center project Information

Center project name: TP43-042C06

Center clone name: RP43-042C06

Center project name: TP63-042C06

Center project name: TP63-042C06

Consensus quality: pVe-terminator Big Dye and ET; 100% of reads Assembly

program: Phrap; version 0.990329

Consensus quality: 176518 bases at least Q40

Consensus quality: 176550 bases at least Q20

Consensus quality: 176577 bases at least Q20
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                                          BS000178
Pan troglodytes chromosome 22 clone:RP43-042C06, map 22, complete
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                                                                                                                                                                                                                                                          Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center, Daejeon, Korea;
*Max-Planck-Institute for Molecular Genetics, Berlin, Germany;
*National Institute of Genetics, Mishima, Japan;
*National Yang Ming University Genome Research Center, Taipei,
                                                                                                                                                                                                                                                                                                                                                                          evolutionary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an attempt was made to resolve all sequencing problems, such compressions and repeats, all regions were covered by at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clones may be obtained from Asao Fujiyama and co-workers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                       The Chimpanzee Chromosome 22 Sequencing Consortium. DNA sequence of chimpanzee chromosome 22 and its evimplications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.gsc.riken.go.jp).
VBCTOR: pBACe3.6
Sequence Quality Assessment:
This entry has been annotated with sequence
                                                                                                                                                                                                             Pan troglodytes (chimpanzee)
                                                                                                                                                       BS000178.1 GI:37537445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality coverage: 9.0x
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                                                                                                                                                                                                                                            Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   code: CHGCS
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RESULT 11
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214890 ACAGTGGCTGTCACTGTCATGCCTCAGTGGAGAGTGTCGGGCCTTCATTGAAAACAACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214710 AGAGGACTGATGTGCTGCTTCCGTGATGTCCTTCTTGGCTTTCATGATGGCCATCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThralaGlyIleIlePheIleIleThrGlyMetValValLeuIleProValSerTrpVal
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  /rpt_family="Simple_repeat"
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Best Local Similarity:
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Direct (26-MAY-2003) Shengyue Wang, Chinese National Human Submitted (26-MAY-2003) Shengyue Wang, Chinese National Human Genome Center at Shanghai, Genomic Sequencing; No.250 BiBo Road, Zhang Jang HI-TECH Park, Shanghai 201203, CHINA (E-mail:wangsy@chgc.sh.cn, URL:http://www.chgc.sh.cn, Tel:86-21-50801919, Fax:86-21-50801922)
The Chimpanzee Chromosome 22 Sequencing Consortium consists of:
*Chinese National Human Genome Center at Shanghai, Shanghai, China;
*Chinese National Human Genome Center at Shanghai, Shanghai, China;
*GENF. Dept. of Genome Analysis, Braunschweig, Germany; *Institute of Molecular Biotechnology, Jena, Germany; *KRIBB Genome Research Center, Daejeon, Korea;
*Max-Planck-Institute of Genetics, Mishima, Japan;
*National Institute of Genetics, Mishima, Japan;
*National Yang Ming University Genome Research Center, Taipei,
                                                                                                                                             bp DNA linear PRI 07-OCT-2003
2 clone:PTB-118H03, map 22, complete
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Chimpanzee Chromosome 22 Sequencing Consortium.

DNA sequence of chimpanzee chromosome 22 and its evolutionary implications

Unpublished

2 (bases 1 to 267172)

Wang, S., Cai, Z., Wang, B., Zheng, H., Zhang, Y., Zhang, X., Zhu, G., Lu, G., Fu, G. and Chen, Z.

Direct Submission
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------ Genome Center
Center: Chinese National Human Genome Center at Shanghai Center
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(http://www.gsc.riken.go.jp).
VBCTOR: pKS145
VBCTOR: coulity Assessment:
This entry has been annotated with sequence
                                                                                                                                                 BS000177 267172 b
Pan troglodytes chromosome 22
                                                                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes (chimpanzee)
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                                                                                                                                                                                                                                                                                                                               GI:37537444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10808 GGCATGAATGCACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGTCAAGGTCAAGGTCAAGGTGAAGGTCAAGGTCAAGGTGAAGGTGAAGGTGAAGGTCAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGAAGGTAAGGTGAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAA
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estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetAlaThrHisAlaLeuGluIleAlaGlyLeuDheLeuGlyGlyValGlyMetValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31108 ATGGCAACCCACGCCTTAGAAATCGCTGGGCTGTTTCTTGGTGGTGTTGGAATGGTGGTG
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                                                                                                                                                                                                                                            Neighboring clones: PTB-118H03(left) and RP43-082J09(right)
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                                                                                                                                                                                                                                                                        Location/Qualifiers
1. 176580
| Organism="Pen troglodytes" |
| Ab xref="taxon:9598" |
| Chromosome="2" |
| Clrome="RP43" |
| Clone="RP43" |
| Clone="RP44" |
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estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error 10,000 bp.
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                                                           and RP43-042C06 (right)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Location/Qualifiers
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Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primers for synthesising full-length cDNA and their use Patent: EP 1074617-A 1588 07-FEB-2001; Patent: EP 1074617-A 1588 07-FEB-2001; Patent: Docation for Biotechnology (JP)
        17-DEC-2003
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                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches:
Conservative:
Mismatches:
Indels:
          DNA
837 bp DN Sequence 1588 from Patent EP1074617.

    .837
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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1140.00
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97.79%
                                                                                                         Homo sapiens (human)
Homo sapiens
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	APOUL846 LOCUS LOCUS Homo sapiens chromosome 18 clone RP11-796C24 map 18q22, WORKING DEFINITION Homo sapiens chromosome 18 clone RP11-796C24 map 18q22, WORKING APOUL846 VERSION VERSION RAPOUL846. GI:8117509 REAWORDS HOMO sapiens (human) OURANISM Homo sapiens (human) Mammalia: Eutheria: Primares; Cararhini; Hominidae; Homo. Mammalia: Eutheria: Primares; Cararhini; Hominidae; Mammalia: Eutheria: Primares; Mammalia: Primares; Mam
CTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGACAGTAGCTACAGATACTCGATACCT SerHishYGThrThrGInLySSerTYTHisThrGINLySSer-ProSerValTyrSe 2	CI2N15/09, CO7K14/47, CO7K16/18, CI2N1/15, CI2N1/19, CI2N1/21, CI2N5/ PC TO CI2P21/02, CI2Q1/68/CI2P21/08, G06F17/30, CI2N15/00, CI2NS/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key FT

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NOTE: This is a 'working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 167257 bases at least 040 Consensus quality: 178235 bases at least 020 Consensus quality: 183393 bases at least 020 Insert aize: 186425; sum-of-contigs Quality coverage: 4.34x in Q20 bases; sum-of-contigs
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It currently

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consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                contig of 10920 bp in length contig of 109 bp in length is gap of 100 bp contig of 8813 bp in length contig of 8813 bp in length is contig of 8622 bp in length is gap of 100 bp in length is gap of 100 bp in length is contig of 6930 bp in length is gap of 100 bp in
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* 149974 151895: contig of 1922 bp in length	4.45e-116 Leng 1134.00 Matc 98.67% Cons 98.67% Mism 96.76% Inde	US-10-063-732-120 (1-225) x AP001846 (1-191923) OY	Oy 21 ThrvalAlava!ThrvalMetProGlnTrpArgvalSerAlaPhelleGluAsnAsnile 40	Qy 41 ValValPheGluAsnPheTrpGluGlyLeuTrpMetAsnCysValArgGlnAlaAsnIle 60	Qy 61 ArgMetGlnCysLysIleTyrAspSerLeuLeuAlaLeuSerProAspLeuGlnAlaAla 80	Qy 81 ArgGlyLeuMetCysAlaAlaSerValMetSerPheLeuAlaPheWetMetAlaIleLeu 100	Oy 101 GlyMetLysCysThrArgCysThrGlyAspAsnGluLysValLysAlaHisIleLeuLeu 120 Db 129709 GGCATGAAATGCACCAGGTGCACGAGCACAATGAGAAGGCTCACATTCTGCTG 129768	Qy 121 ThraladlylleilePheileIleThrGlyMetValValLeuileProValSerTrpVal 140	Oy 141 AlaAsnAlaIleIleArgAspPheTyrAsnSerIleValAsnValAlaGlnLysArgGlu 160 Db 129829 GCCAATGCCATCATCAGAGATTTCTATAACCCAATAGTGATGTTGCCCAAAAGGTGAG 129888	Qy 161 LeuGlyGlualaLeuTyrLeuGlyTrpThrThrAlaLeuValLeuIleValGlyGlyAla 180 Db 129889 CTTGGAGAAGCTCTCTACTTAGAAGGACCACGGCACTGGTGCTGATTGTTGGAGGAGGACCT 129948	Qy 181 LeuPheCysCysValPheCysCysAsnGluLysSerSerSerSerTyrArgTyrSerIlePro 200	Oy 201 SerHisArgThrThrGlnLysSerTyrHisThrGlyLysLysSerProSerValTyrSer 220

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Search completed: September 3, 2004, 04:36:28 Job time: 2908 secs